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OM nucleic - nucleic search, using sw model

Run on: May 19, 2004, 02:49:51 ; Search time 74 Seconds
(without alignments)
427.462 Million cell updates/sec

Title: RIBOZYME1A

Perfect score: 57

Sequence: 1 ggguccaccuccgcggun.....uucgcauggcuaggagccc 57

Scoring table: IDENTITY NUCDX

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents NA.*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	54.4	61	1	US-08-238-963A-18
2	29.6	51.9	52	1	US-08-741-881-40
3	29.6	51.9	52	1	US-08-741-881-80
4	29.6	51.9	52	1	US-08-739-158-40
5	29.6	51.9	52	1	US-08-739-158-80
6	29.6	51.9	52	2	US-08-739-167-40
7	29.6	51.9	52	2	US-08-739-167-80
8	29.6	51.9	52	3	US-08-404-796-40
9	29.6	51.9	52	3	US-08-404-796-80
10	29.6	51.9	52	3	US-08-931-869-40
11	29.6	51.9	52	3	US-08-931-869-80
12	29.6	51.9	52	4	US-09-350-399-40
13	29.6	51.9	52	4	US-09-350-399-80
14	29.6	51.9	52	4	US-09-236-140A-40
15	29.6	51.9	52	4	US-09-236-140A-80
16	29.6	51.9	80	1	US-08-238-963A-16
17	29.6	51.9	83	3	US-08-646-695-12
18	29.6	51.9	83	5	PCT-US96-06053-12
19	29.6	51.9	84	1	US-08-238-963A-13
20	29.6	51.9	84	1	US-08-238-963A-14
21	29.6	51.9	86	1	US-08-238-963A-6
22	29.6	51.9	90	4	US-09-554-337-2
23	29.6	51.9	90	4	US-09-733-042-12
24	29.6	51.9	90	4	US-09-733-042-13
25	29.6	51.9	101	6	5225337-2
26	29.6	51.9	105	2	US-08-553-619B-25
27	29.6	51.9	105	2	US-08-553-619B-30

28	29.6	51.9	8100	4	US-09-554-337-4	Sequence 4, Appli
29	29.6	51.9	14311	3	US-08-646-695-1	Sequence 1, Appli
c 30	29.6	51.9	14311	3	US-08-646-695-7	Sequence 7, Appli
31	29.6	51.9	14311	5	PCT-US96-06053-1	Sequence 1, Appli
c 32	29.6	51.9	14311	5	PCT-US96-06053-7	Sequence 7, Appli
33	29.6	51.9	15538	4	US-09-554-337-1	Sequence 1, Appli
c 34	29.6	51.2	601	4	US-09-814-951A-6	Sequence 6, Appli
c 35	29.2	51.2	1445	4	US-09-814-951A-1	Sequence 1, Appli
c 36	29.2	51.2	9704	4	US-09-814-951A-3	Sequence 3, Appli
37	28.8	50.5	85	1	US-08-238-963A-12	Sequence 12, Appli
38	28.4	49.8	1197	4	US-09-579-182-1	Sequence 1, Appli
c 39	28.4	49.8	1600	3	US-08-602-791-1	Sequence 1, Appli
c 40	28.4	49.8	3386	3	US-09-041-886-1	Sequence 1, Appli
41	28.2	49.5	56	4	US-09-415-785A-39	Sequence 39, Appli
42	28.2	49.5	56	4	US-09-415-785A-39	Sequence 39, Appli
43	28.2	49.5	56	4	US-09-415-868-39	Sequence 39, Appli
44	28.2	49.5	56	4	US-09-415-868-39	Sequence 39, Appli
45	28.2	49.5	56	4	US-09-415-900-39	Sequence 39, Appli

ALIGNMENTS

RESULT 1
US-08-238-963A-18
; Sequence 18, Application US/08238963A
; Patent No. 5625047
; GENERAL INFORMATION:
; APPLICANT: Been, Michael D.
; APPLICANT: Rosenstein, Sarah P.
; APPLICANT: Perrotta, Anne T.
; TITLE OF INVENTION: ENZYMAIC RNA MOLECULES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA: US/08/238,963A
; APPLICATION NUMBER: US/08/238,963A
; FILING DATE: May 5, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/821,155
; FILING DATE: January 13, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 207/093
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-238-963A-18

Query Match 54.4%; Score 31; DB 1; Length 61;
Best Local Similarity 77.4%; Pred. No. 1.4;
Matches 41; Conservative 6; Mismatches 2; Indels 4; Gaps 1;

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; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/741,881
; FILING DATE: 30-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McMahsters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423C6 / 1146.007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-741-881-80

Query Match 51.9%; Score 29.6; DB 1; Length 52;
Best Local Similarity 59.4%; Pred. No. 3.7;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCCGCGGUNNNDNNUGGCAUGCGCUUCCGAUGCUAAGGACC 35
; :||||:||||:||||:||||:||||:||||:
Db 1 TCCACCTCTCGCGGTCGACCTGGGCATCCG 32

RESULT 4
US-08-739-158-40
; Sequence 40, Application US/08739158
; Patent No. 5814482
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/739,158
; FILING DATE: 30-OCT-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: McMahsters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423D3 / 1146.012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-741-881-40

Query Match 51.9%; Score 29.6; DB 1; Length 52;
Best Local Similarity 59.4%; Pred. No. 3.7;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCCGCGGUNNNDNNUGGCAUGCGCUUCCGAUGCUAAGGACC 35
; :||||:||||:||||:||||:||||:||||:
Db 1 TCCACCTCTCGCGGTCGACCTGGGCATCCG 32

RESULT 3
US-08-741-881-80
; Sequence 80, Application US/08741881
; Patent No. 5789245
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/741,881
; FILING DATE: 30-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McMahsters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423C6 / 1146.007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-741-881-40

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TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 52 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-739-158-40

Query Match 51.9%; Score 29.6; DB 1; Length 52;
Best Local Similarity 59.4%; Pred. No. 3.7;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

Qy 4 UCCACCUCCGCGGNNNNNUGGCGAUGC 35
Db 1 TCCACCTCTCGCGTCCGACCTGGGCATCCG 32

RESULT 5

US-08-739-158-80
Sequence 80, Application US/08739158
Patent No. 5814482

GENERAL INFORMATION:
APPLICANT: Dubensky Jr., Thomas W
APPLICANT: Polo, John M.
APPLICANT: Ibanez, Carlos E.
APPLICANT: Chang, Stephen M.W.
APPLICANT: Jolly, Douglas J.
APPLICANT: Driver, David A.
TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/739.158
FILING DATE: 30-OCT-1996
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.423D3 / 1146.012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 52 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-739-158-80

Query Match 51.9%; Score 29.6; DB 1; Length 52;
Best Local Similarity 59.4%; Pred. No. 3.7;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

Qy 4 UCCACCUCCGCGGNNNNNUGGCGAUGC 35
Db 1 TCCACCTCTCGCGTCCGACCTGGGCATCCG 32

RESULT 6

US-08-739-167-40
Sequence 40, Application US/08739167

Patent No. 5843723
GENERAL INFORMATION:
APPLICANT: Dubensky Jr., Thomas W
APPLICANT: Polo, John M.
APPLICANT: Ibanez, Carlos E.
APPLICANT: Chang, Stephen M.W.
APPLICANT: Jolly, Douglas J.
APPLICANT: Driver, David A.
APPLICANT: Belli, Barbara A.
TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS AND ALPHAVIRUS
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/739.167
FILING DATE: 30-OCT-1996
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.423C7 / 1146.008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 52 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-739-167-40

Query Match 51.9%; Score 29.6; DB 2; Length 52;
Best Local Similarity 59.4%; Pred. No. 3.7;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

Qy 4 UCCACCUCCGCGGNNNNNUGGCGAUGC 35
Db 1 TCCACCTCTCGCGTCCGACCTGGGCATCCG 32

RESULT 7

US-08-739-167-80
Sequence 80, Application US/08739167
Patent No. 5843723

GENERAL INFORMATION:
APPLICANT: Dubensky Jr., Thomas W
APPLICANT: Polo, John M.
APPLICANT: Ibanez, Carlos E.
APPLICANT: Chang, Stephen M.W.
APPLICANT: Jolly, Douglas J.
APPLICANT: Driver, David A.
APPLICANT: Belli, Barbara A.
TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS AND ALPHAVIRUS
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/739.167
FILING DATE: 30-OCT-1996
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.423C7 / 1146.008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 52 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-739-167-80

/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ FILING DATE: 30-OCT-1996
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: McMaisters, David D.
/ REGISTRATION NUMBER: 33,963
/ REFERENCE/DOCKET NUMBER: 930049.423C7 / 1146.008
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206) 622-4900
/ TELEFAX: (206) 682-6031
/ INFORMATION FOR SEQ ID NO: 80:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 52 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-739-167-80

Query Match 51.9%; Score 29.6; DB 2; Length 52;
Best Local Similarity 59.4%; Pred. No. 3.7;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCCGCGGUNNNNUGGCGCAUGCG 35
DB 1 TCCACCTCTCGCGTCCGACCTGGGCATCCG 32

RESULT 8

US-08-404-796-40
/ Sequence 40, Application US/08404796
/ Patent No. 6015686
/ GENERAL INFORMATION:
/ APPLICANT: Dubensky Jr, Thomas W
/ APPLICANT: Polo, John M.
/ APPLICANT: Ibanez, Carlos E.
/ APPLICANT: Chang, Stephen M.W.
/ APPLICANT: Jolly, Douglas J.
/ APPLICANT: Driver, David A.
/ APPLICANT: Belli, Barbara A.
/ TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
/ NUMBER OF SEQUENCES: 128
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: SEED and BERRY LLP
/ STREET: 6300 Columbia Center, 701 Fifth Avenue
/ CITY: Seattle
/ STATE: Washington
/ COUNTRY: US
/ ZIP: 98104-7092
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ FILING DATE: 15-MAR-1995
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: McMaisters, David D.
/ REGISTRATION NUMBER: 33,963
/ REFERENCE/DOCKET NUMBER: 930049.423C5 / 1146.006
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206) 622-4900
/ TELEFAX: (206) 682-6031
/ INFORMATION FOR SEQ ID NO: 40:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 52 base pairs
/ TYPE: nucleic acid

/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-404-796-40

Query Match 51.9%; Score 29.6; DB 3; Length 52;
Best Local Similarity 59.4%; Pred. No. 3.7;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCCGCGGUNNNNUGGCGCAUGCG 35
DB 1 TCCACCTCTCGCGTCCGACCTGGGCATCCG 32

RESULT 9

US-08-404-796-80
/ Sequence 80, Application US/08404796
/ Patent No. 6015686
/ GENERAL INFORMATION:
/ APPLICANT: Dubensky Jr, Thomas W
/ APPLICANT: Polo, John M.
/ APPLICANT: Ibanez, Carlos E.
/ APPLICANT: Chang, Stephen M.W.
/ APPLICANT: Jolly, Douglas J.
/ APPLICANT: Driver, David A.
/ APPLICANT: Belli, Barbara A.
/ TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
/ NUMBER OF SEQUENCES: 128
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: SEED and BERRY LLP
/ STREET: 6300 Columbia Center, 701 Fifth Avenue
/ CITY: Seattle
/ STATE: Washington
/ COUNTRY: US
/ ZIP: 98104-7092
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA: US/08/404,796
/ FILING DATE: 15-MAR-1995
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: McMaisters, David D.
/ REGISTRATION NUMBER: 33,963
/ REFERENCE/DOCKET NUMBER: 930049.423C5 / 1146.006
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206) 622-4900
/ TELEFAX: (206) 682-6031
/ INFORMATION FOR SEQ ID NO: 80:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 52 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-404-796-80

Query Match 51.9%; Score 29.6; DB 3; Length 52;
Best Local Similarity 59.4%; Pred. No. 3.7;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCCGCGGUNNNNUGGCGCAUGCG 35
DB 1 TCCACCTCTCGCGTCCGACCTGGGCATCCG 32

RESULT 10

US-08-931-869-40
/ Sequence 40, Application US/08931869
/ Patent No. 6015694
/ GENERAL INFORMATION:
/ APPLICANT: Dubensky Jr, Thomas W

APPLICANT: Polo, John M.
APPLICANT: Ibanez, Carlos E.
APPLICANT: Chang, Stephen M.W.
APPLICANT: Jolly, Douglas J.
APPLICANT: Driver, David A.
APPLICANT: Belli, Barbara A.
TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/931,869
FILING DATE: 16-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/404,796
FILING DATE: 15-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.423C5 / 1146.006
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 52 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-931-869-40

Query Match 51.9%; Score 29.6; DB 3; Length 52;
Best Local Similarity 59.4%; Pred. No. 3.7;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

Qy 4 UCCACCTCCGCGGNNNNUGGCGAUGC 35
Db 1 TCCACCTCCGCGGTCGACCTGGCATCCG 32

RESULT 11

US-08-931-869-80
Sequence 80, Application US/08931869
Patent No. 6015694
GENERAL INFORMATION:
APPLICANT: Dubensky Jr, Thomas W
APPLICANT: Polo, John M.
APPLICANT: Ibanez, Carlos E.
APPLICANT: Chang, Stephen M.W.
APPLICANT: Jolly, Douglas J.
APPLICANT: Driver, David A.
APPLICANT: Belli, Barbara A.
TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/350,399
FILING DATE: 08-Jul-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.423D1 / 1146.010
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 52 base pairs
TYPE: nucleic acid

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/931,869
FILING DATE: 16-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/404,796
FILING DATE: 15-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.423C5 / 1146.006
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 52 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-931-869-80

Query Match 51.9%; Score 29.6; DB 3; Length 52;
Best Local Similarity 59.4%; Pred. No. 3.7;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

Qy 4 UCCACCTCCGCGGNNNNUGGCGAUGC 35
Db 1 TCCACCTCCGCGGTCGACCTGGCATCCG 32

RESULT 12

US-09-350-399-40
Sequence 40, Application US/09350399
Patent No. 6342372
GENERAL INFORMATION:
APPLICANT: Dubensky Jr, Thomas W
APPLICANT: Polo, John M.
APPLICANT: Jolly, Douglas J.
APPLICANT: Driver, David A.
TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/350,399
FILING DATE: 08-Jul-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.423D1 / 1146.010
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 52 base pairs
TYPE: nucleic acid

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;
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-09-350-399-40

Query Match      51.9%; Score 29.6; DB 4; Length 52;
Best Local Similarity 59.4%; Pred. No. 3.7;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCCGCGGUNNNNNUGGCGAUGC 35
DB 1 TCCACCTCTCGCGTCCGACCTGGGCATCCG 32

RESULT 13
US-09-350-399-80
; Sequence 80, Application US/09350399
; Patent No. 6342372
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; Polo, John M.
; Jolly, Douglas J.
; Driver, David A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/350,399
; FILING DATE: 08-Jul-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423D1 / 1146.010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 80:
US-09-350-399-80

Query Match      51.9%; Score 29.6; DB 4; Length 52;
Best Local Similarity 59.4%; Pred. No. 3.7;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCCGCGGUNNNNNUGGCGAUGC 35
DB 1 TCCACCTCTCGCGTCCGACCTGGGCATCCG 32

RESULT 14
US-09-236-140A-40
; Sequence 40, Application US/09236140A
; Patent No. 6378236
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; Polo, John M.
; Ibanez, Carlos E.
; Chang, Stephen M.W.
; Jolly, Douglas J.
; Driver, David A.
; Belli, Barbara A.
; TITLE OF INVENTION: RECOMBINANT ALPHAVIRUS PARTICLES
; NUMBER OF SEQUENCES: 124
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OPPENHEIMER WOLFF & DONNELLY
; STREET: 840 NEWPORT CENTER DRIVE, SUITE 700
; CITY: NEWPORT BEACH
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
```

```
;
; Ibanez, Carlos E.
; Chang, Stephen M.W.
; Jolly, Douglas J.
; Driver, David A.
; Belli, Barbara A.
; TITLE OF INVENTION: RECOMBINANT ALPHAVIRUS PARTICLES
; NUMBER OF SEQUENCES: 124
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OPPENHEIMER WOLFF & DONNELLY
; STREET: 840 NEWPORT CENTER DRIVE, SUITE 700
; CITY: NEWPORT BEACH
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/236,140A
; FILING DATE: 22-Jan-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Cullman, Louis C.
; REGISTRATION NUMBER: 39,645
; REFERENCE/DOCKET NUMBER: 20263.332 / 1146.020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (949) 823.6000
; TELEFAX: (949) 823.6100
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-09-236-140A-40

Query Match      51.9%; Score 29.6; DB 4; Length 52;
Best Local Similarity 59.4%; Pred. No. 3.7;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCCGCGGUNNNNNUGGCGAUGC 35
DB 1 TCCACCTCTCGCGTCCGACCTGGGCATCCG 32

RESULT 15
US-09-236-140A-80
; Sequence 80, Application US/09236140A
; Patent No. 6378236
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; Polo, John M.
; Ibanez, Carlos E.
; Chang, Stephen M.W.
; Jolly, Douglas J.
; Driver, David A.
; Belli, Barbara A.
; TITLE OF INVENTION: RECOMBINANT ALPHAVIRUS PARTICLES
; NUMBER OF SEQUENCES: 124
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OPPENHEIMER WOLFF & DONNELLY
; STREET: 840 NEWPORT CENTER DRIVE, SUITE 700
; CITY: NEWPORT BEACH
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/236,140A
; FILING DATE: 22-Jan-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Cullman, Louis C.
; REGISTRATION NUMBER: 39,645
; REFERENCE/DOCKET NUMBER: 20263.332 / 1146.020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (949) 823.6000
; TELEFAX: (949) 823.6100
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 80:
US-09-236-140A-80

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Query Match      51.9%; Score 29.6; DB 4; Length 52;
Best Local Similarity 59.4%; Pred. No. 3.7;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

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Qy      4 UCCACUCCUGCGGUNNDNNUGGCGAUGC 35
Db      1 TCCACCTCTCGCGTCCGACCTGGGCATCCG 32

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Search completed: May 19, 2004, 04:52:40
Job time : 88 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model
Run on: May 19, 2004, 02:46:06 ; Search time 3211 Seconds
(without alignments)
530.098 Million cell updates/sec

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Perfect score: 57
Sequence: 1 ggguccaccuccgcggun.....ucgcaggcuaggagccc 57

Scoring table: IDENTITY_NUCDX
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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16: em_estom.*
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20: em_gss_vrt.*
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29: gb_gss2.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
c 1	32.2	56.5	857	14	CF552723
c 2	32	56.1	1182	12	BI457296
c 3	31.4	55.1	622	29	CC526419
c 4	30.6	53.7	869	14	CB991305

5	30.2	53.0	382	10	AW681122	AW681122 WS1_8_E02
6	30.2	53.0	405	10	AW681043	AW681043 WS1_8_E02
7	30.2	53.0	448	10	AW283452	AW283452 LGI_272_E
8	30.2	53.0	726	10	BF686394	BF686394 602143774
9	30.2	53.0	807	10	BE902113	BE902113 601674890
10	29.8	52.3	538	10	BE682984	BE682984 181389 MA
c 11	29.8	52.3	777	10	BF796052	BF796052 602259070
c 12	29.8	52.3	808	12	BM006402	BM006402 603615114
c 13	29.8	52.3	823	29	CC593873	CC593873 CH240_395
c 14	29.4	51.6	495	12	BJ004361	BJ004361 BJ004361
c 15	29.4	51.6	513	10	BE386169	BE386169 601274411
c 16	29.4	51.6	1057	12	BM553956	BM553956 AGENCOURT
c 17	29.2	51.2	123	9	AU077016	AU077016 AU077016
c 18	29.2	51.2	222	14	CF122359	CF122359 UI-HF-CB0
c 19	29.2	51.2	257	12	BM798569	BM798569 K-EST0082
c 20	29.2	51.2	300	9	AU099987	AU099987 AU099987
c 21	29.2	51.2	349	14	CB126416	CB126416 K-EST0175
c 22	29.2	51.2	370	9	AL701336	AL701336 DKF2D686L
c 23	29.2	51.2	380	14	CB144469	CB144469 K-EST0198
c 24	29.2	51.2	428	14	CF144607	CF144607 UI-HF-CB0
c 25	29.2	51.2	453	12	BM836423	BM836423 K-EST0112
c 26	29.2	51.2	453	14	CB126144	CB126144 K-EST0175
c 27	29.2	51.2	457	14	CF135198	CF135198 UI-HF-CB0
c 28	29.2	51.2	481	14	CB113346	CB113346 K-EST0155
c 29	29.2	51.2	487	9	AW004672	AW004672 W991F12.X
c 30	29.2	51.2	496	14	CB125500	CB125500 K-EST0174
c 31	29.2	51.2	496	14	CB127743	CB127743 K-EST0177
c 32	29.2	51.2	501	10	BE386170	BE386170 601274413
c 33	29.2	51.2	503	10	BE269642	BE269642 601185048
c 34	29.2	51.2	507	14	CB140642	CB140642 K-EST0194
c 35	29.2	51.2	508	10	BE296622	BE296622 601173643
c 36	29.2	51.2	511	12	BI053587	BI053587 MR3-GN046
c 37	29.2	51.2	513	14	CB141699	CB141699 K-EST0195
c 38	29.2	51.2	513	28	AQ294266	AQ294266 HS_3009_A
c 39	29.2	51.2	516	10	BE296669	BE296669 601174409
c 40	29.2	51.2	516	14	CB114356	CB114356 K-EST0157
c 41	29.2	51.2	519	14	CB125200	CB125200 K-EST0173
c 42	29.2	51.2	529	14	CB125108	CB125108 K-EST0173
c 43	29.2	51.2	529	14	CB146530	CB146530 K-EST0201
c 44	29.2	51.2	533	10	BF304959	BF304959 601888662
c 45	29.2	51.2	536	14	CB126208	CB126208 K-EST0175

ALIGNMENTS

RESULT 1
CF552723/c
LOCUS
DEFINITION
AGENCOURT_15595333 NIH_MGC_183 Homo sapiens cDNA clone
IMAGE:30529107 5', mRNA sequence.
CF552723
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1 (bases 1 to 857)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
cDNA Library Preparation: Invitrogen Corp
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

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http://image.llnl.gov
Plate: NDAM616 row: c column: 04
High quality sequence stop: 680.
FEATURES
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            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGE:30529107"
            /lab_host="DH10B-Tona (T1 and T5 phage resistant)"
            /clone_lib="NIH_MGC_183"
            /note="Organ: Pooled muscle (cardiac and skeletal);
            Vector: pCMV-SPORT6.1; Site 1: EcoRV (destroyed); Site 2:
            NotI; Library is oligo-dT primed and directionally cloned
            (EcoRV site is destroyed upon cloning). Average insert
            size 1.7. Library was constructed by Invitrogen."
ORIGIN
    Query Match      56.5%; Score 32.2; DB 14; Length 857;
    Best Local Similarity 50.9%; Pred. No. 1e+03;
    Matches 29; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

Qy 1 GGGUCCACUCUCGCGGNNNNNUGGCGAUGCGGUUCGCAUGGCUAAGGACCC 57
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 178 GGGTCTCTCTCGGAGACCTTGTGTCTCATGGCGCTGCGGTGTGAGCGGCC 122
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RESULT 2
BI457296/c          1182 bp mRNA linear EST 21-AUG-2001
LOCUS               603185617F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:5258380 5',
DEFINITION          mRNA sequence.
ACCESSION            BI457296
VERSION              BI457296.1 GI:15247965
KEYWORDS
SOURCE
ORGANISM             Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1182)
AUTHORS              NIH-MGC http://mgc.nci.nih.gov/.
TITLE                National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL              Unpublished (1999)
COMMENT              Contact: Robert Strausberg, Ph.D.
                    Email: cgabbs@mail.nih.gov
                    Tissue Procurement: ATCC
                    cDNA Library Preparation: Ling Hong/Rubin Laboratory
                    cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                    DNA Sequencing by: Incyte Genomics, Inc.
                    Clone distribution: MGC clone distribution information can be
                    found through the I.M.A.G.E. Consortium/LLNL at:
                    http://image.llnl.gov
                    Plate: LLCM1870 row: a column: 05
                    High quality sequence stop: 335.
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            /lab_host="DH10B (phage-resistant)"
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            /note="Organ: pancreas; Vector: pOTB7; Site 1: XhoI;
            Site 2: EcoRI; cDNA made by oligo-dT priming.
            Directionally cloned into EcoRI/XhoI sites using the
            following 5' adaptor: GGCACGAG(G). Size-selected >500bp
            for average insert size 1.8kb. Library constructed by Ling
            Hong in the laboratory of Gerald M. Rubin (University of
            California, Berkeley) using ZAP-cDNA synthesis kit
            (Stratagene) and Superscript II RT (Life Technologies).
            Note: this is a NIH_MGC Library."
ORIGIN

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Query Match      56.1%; Score 32; DB 12; Length 1182;
Best Local Similarity 52.3%; Pred. No. 1.3e+03;
Matches 23; Conservative 14; Mismatches 7; Indels 0; Gaps 0;

Qy 4 UCCACUUCUCGCGGNNNNNUGGCGAUGCGGUUCGCAUGGC 47
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Db 827 TCCTCGTCTCGCGGTGGTGTGGATTGCGGTGCTGCGGC 784
    |||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 3
CC526419           622 bp DNA linear GSS 17-JUN-2003
LOCUS              CH240_401C15.TARBAC13P2 CHORI-240 Bos taurus genomic clone
DEFINITION          CH240_401C15, genomic survey sequence.
ACCESSION            CC526419
VERSION              CC526419.1 GI:31844707
KEYWORDS
SOURCE              GSS.
ORGANISM             Bos taurus (cow)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 622)
AUTHORS              Holt, R., Stott, J., Yang, G., Barber, S., Smalhus, D., Prabhu, A.-L.,
                    Tsai, M., Cloutier, A., Lee, D., Girn, N., Olson, T., Mayo, M.,
                    Buterfield, Y., Kirkpatrick, R., Liu, J., Guin, R., Chan, A., Chiu, R.,
                    Mathewson, C., Wye, N., Masson, A., Brown-John, M., Jones, S.,
                    Schein, J., Marra, M., de Jong, P., Keefe, J.W. and Kappes, S.M.
                    Bovine BAC End Sequences from Library CHORI-240, PLATES 399 to 478
                    Unpublished (2003)
                    Other GSSs: CH240_401C15.T7
                    Contact: Rob Holt
                    Sequencing
                    The British Columbia Cancer Agency Genome Science Centre
                    600 W. 10th Ave, Vancouver, British Columbia, Canada V5Z 4E6
                    Tel: 604-877-6085
                    Fax: 604-877-6276
                    Email: rholtebcgsc.ca
                    Clones are derived from the bovine BAC library CHORI-240
                    (http://www.chori.org/bacpac/bovine240.htm). For BAC library
                    availability, please contact Pieter de Jong (pdejong@mail.choi.org).
                    Clones may be purchased from BACPAC Resources
                    (http://www.chori.org/bacpac/ordering/information.htm). This work
                    was undertaken as part of the International Bovine BAC Mapping
                    Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the
                    British Columbia Genome Sciences Centre, Canada.
                    Plate: 401 row: C column: 15
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            /clone_lib="CHORI-240"
            /note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI;
            Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC
            library (Male) produced by Pieter de Jong"
ORIGIN
    Query Match      55.1%; Score 31.4; DB 29; Length 622;
    Best Local Similarity 50.9%; Pred. No. 1.5e+03;
    Matches 27; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

Qy 5 CCACUUCUCGCGGNNNNNUGGCGAUGCGGUUCGCAUGGCUAAGGACCC 57
    |||:|||||:|||||:|||||:|||||:|||||:|||||
Db 104 CTCCTCTCTCGGTGGTGGCGGTGCATCTCCACCTCCCTCAGGCCCC 156
    |||:|||||:|||||:|||||:|||||:|||||:|||||

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REFERENCE
AUTHORS
TITLE
JOURNAL
1 (bases 1 to 807)
NTH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

```

COMMENT      Contact: Robert Strausberg, Ph.D.
              Email: cgapbs-remail.nih.gov
              Tissue Procurement: ATCC
              cDNA Library Preparation: Ling Hong/Rubin Laboratory
              cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: Incyte Genomics, Inc.
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
              Plate: LLCM835 row: d column: 24
              High quality sequence stop: 778.

FEATURES
  source
    1..807
      /organism="Homo sapiens"
      /mol_type="mRNA"
      /db_xref="taxon:9606"
      /clone="IMAGE:3957479"
      /tissue_type="choriocarcinoma"
      /lab_host="DH10B (phage-resistant)"
      /clone_lib="NIH_MGC_21"
      /note="Organ: placenta; Vector: pOTB7; Site 1: XhoI;
      Site 2: EcoRI; cDNA made by oligo-dT priming.
      Directionally cloned into EcoRI/XhoI sites using the
      following 5' adaptor: GGCACGAG(G). Size-selected >500bp
      for average insert size 1.8Kb. Library constructed by
      Ling Hong in the laboratory of Gerald M. Rubin (University
      of California, Berkeley) using ZAP-cDNA synthesis kit
      (Stratagene) and Superscript II RT (Life Technologies)."
```

Query Match 53.0%; Score 30.2; DB 10; Length 807;
 Best Local Similarity 54.9%; Pred. No. 3.5e+03;
 Matches 28; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

Qy 2 GGUCCACUCCUGCGGUNNNDNUGGCAUGCGGCUUGCAUGCUAAGG 52
 Db 624 GCTGCCACCTGGCTGCTGTCATAGGGCGGCGCTGCACATGCCAGG 674

```

RESULT 10
LOCUS      BE682984                      538 bp    mRNA    linear    EST 25-APR-2001
DEFINITION 181389 MARC 4BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION  BE682984
VERSION     BE682984.1 GI:10069395
KEYWORDS   EST.
SOURCE      Bos taurus (cow)
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovinae; Bos.
REFERENCE   Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
            Casas,E., Wray,J.E., White,J., Cho,J., Fahrrenkrug,S.C.,
            Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A.,
            Chitko-McKown,C.G., Perteau,G., Holt,I., Karamycheva,S., Liang,F.,
            Quackenbush,J. and Keele,J.W.
            Sequence evaluation of four pooled-tissue normalized bovine cDNA
            libraries and construction of a gene index for cattle
            Genome Res. 11 (4), 626-630 (2001)
JOURNAL     21180013
MEDLINE     11282978
PUBMED
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and alt trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 18
            and -minmatch 12 options.
            PCR Primers
            FORWARD: AGGAACAGCTATGACCAT
            BACKWARD: GTTTTCCAGTCACGAG
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Plate: 84 row: 0 column: 20
 Seq primer: ATTAGGTGCACACTATAG.

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FEATURES
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      /db_xref="taxon:9913"
      /tissue_type="pooled"
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      /clone_lib="MARC 4BOV"
      /note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
      Library made from pooled tissue from day 20 and day 40
      embryos."
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Query Match 52.3%; Score 29.8; DB 10; Length 538;
 Best Local Similarity 46.7%; Pred. No. 3.8e+03;
 Matches 21; Conservative 15; Mismatches 9; Indels 0; Gaps 0;

Qy 4 UCCACUCCUGCGGUNNNDNUGGCAUGCGGCUUGCAUGGCU 48
 Db 393 TGCACCTCCCTGAGCTTCTCGTGGGCTTGCGAGCTTCCCTGGCT 437

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RESULT 11
LOCUS      BF796052                      777 bp    mRNA    linear    EST 12-JAN-2001
DEFINITION 602259070F1 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:4342409 5',
            mRNA sequence.
ACCESSION  BF796052
VERSION     BF796052.1 GI:12101106
KEYWORDS   EST.
SOURCE      Homo sapiens (human)
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   NIH-MGC http://mgi.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: Louis Staudt, M.D., Ph.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: L1AM9957 row: k column: 18
            High quality sequence stop: 716.
FEATURES
  source
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      /organism="Homo sapiens"
      /mol_type="mRNA"
      /db_xref="taxon:9606"
      /clone="IMAGE:4342409"
      /tissue_type="lymphoma, cell line"
      /lab_host="DH10B (phage-resistant)"
      /clone_lib="NIH_MGC_85"
      /note="Organ: lymph; Vector: pCMV-SPORT6; Site 1: NotI;
      Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
      Average insert size 1.867 kb. Library enriched for
      full-length clones and constructed by Life Technologies.
      Note: this is a NIH_MGC Library."
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Query Match 52.3%; Score 29.8; DB 10; Length 777;
 Best Local Similarity 50.9%; Pred. No. 4.5e+03;
 Matches 27; Conservative 12; Mismatches 14; Indels 0; Gaps 0;

Qy 4 UCCACUCCUGCGGUNNNDNUGGCAUGCGGCUUGCAUGGCUAAGGACC 56
 Db 393 TGCACCTCCCTGAGCTTCTCGTGGGCTTGCGAGCTTCCCTGGCT 437

```

Db      268  TCCACCTCTCTGCTGAGCACCGCTCTCTGGGGCTTCCATGCGCAGAGGGTCC 216

RESULT 12
BM006402/c
LOCUS   603615114F1 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:5421075 5',
DEFINITION mRNA sequence.
ACCESSION BM006402
VERSION   BM006402.1 GI:16520756
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS  1 (bases 1 to 808)
TITLE    NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL  National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT  Unpublished (1999)
          Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-remail.nih.gov
          Tissue Procurement: ATCC
          cDNA Library Preparation: Ling Hong/Rubin Laboratory
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Incyte Genomics, Inc.
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: LLCM1876 row: 1 column: 04
          High quality sequence stop: 552.
          Location/Qualifiers
            1..808
              /organism="Homo sapiens"
              /mol_type="mRNA"
              /db_xref="taxon:9606"
              /clone="IMAGE:5421075"
              /tissue_type="ductal carcinoma, cell line"
              /lab_host="DH10B (phage-resistant)"
              /clone_lib="NIH MGC 110"
              /note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
              Site_2: EcoRI; cDNA made by oligo-dT priming.
              Directionally cloned into EcoRI/XhoI sites using the
              following 5' adaptor: GGCACGAG(G). Library constructed by
              Ling Hong in the laboratory of Gerald M. Rubin (University
              of California, Berkeley) using ZAP-cDNA synthesis kit
              (Stratagene) and Superscript II RT (Life Technologies).
              Note: this is a NIH_MGC Library."

ORIGIN
Query Match      52.3%; Score 29.8; DB 12; Length 808;
Best Local Similarity 50.9%; Pred. No. 4.5e+03;
Matches 27; Conservative 12; Mismatches 14; Indels 0; Gaps 0;

Qy  4  UCCACCUCCGCGGUNNNDNUGGCAUGCGGCUUCCGCAUGGCUAAGGACC 56
      :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db    256  TCCACCTCTCTGCTGAGCACCGCTCTCTGGGGCTTCCATGCGCAGAGGGTCC 204

RESULT 13
CC593873
LOCUS   CH240_395G6.TARBAC13p2 CHORI-240 Bos taurus genomic clone
DEFINITION CH240_395G6, genomic survey sequence.
ACCESSION CC593873
VERSION   CC593873.1 GI:31954012
KEYWORDS GSS.
SOURCE    Bos taurus (cow)
ORGANISM Bos taurus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
          Bovidae; Bovinae; Bos.
REFERENCE
AUTHORS  1 (bases 1 to 823)
          Holt, R., Stott, J., Yang, G., Barber, S., Smailus, D., Prabhu, A.-L.,

```

```

Tsai, M., Cloutier, A., Lee, D., Girn, N., Olson, T., Mayo, M.,
Butterfield, Y., Kirkpatrick, R., Liu, J., Guin, R., Chan, A., Chiu, R.,
Mathewson, C., Wye, N., Masson, A., Brown-John, M., Jones, S.,
Schein, J., Marra, M., de Jong, P., McWilliam, S., Barris, W.,
Dairymple, B.P. and Tellam, R.
Bovine BAC End Sequences from Library CHORI-240, PLATES 294 to 398
Unpublished (2003)
Other GSSs: CH240_395G6.T7
Contact: Rob Holt
Sequencing
The British Columbia Cancer Agency Genome Science Centre
600 W. 10th Ave, Vancouver, British Columbia, Canada V5Z 4B6
Tel: 604-877-6085
Fax: 604-877-6276
Email: rholt@bcgsc.ca
Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovine240.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/ordering/information.htm). This work
was undertaken as part of the International Bovine BAC Mapping
Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the
British Columbia Genome Sciences Centre, Canada.
Plate: 395 row: G column: 6
Seq primer: SP6
Class: BAC ends.
          Location/Qualifiers
            1..823
              /organism="Bos taurus"
              /mol_type="genomic DNA"
              /strain="bred: Hereford"
              /db_xref="taxon:9913"
              /clone="CH240_395G6"
              /sex="Male"
              /cell_type="Blood"
              /clone_lib="CHORI-240"
              /note="Vector: pTARBAC1.3; Site_1: MboI; Site_2: MboI;
              Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC
              library (Male) produced by Pieter de Jong"

ORIGIN
Query Match      52.3%; Score 29.8; DB 29; Length 823;
Best Local Similarity 46.7%; Pred. No. 4.6e+03;
Matches 21; Conservative 15; Mismatches 9; Indels 0; Gaps 0;

Qy  4  UCCACCUCCGCGGUNNNDNUGGCAUGCGGCUUCCGCAUGGCU 48
      :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db    512  TGCACCTCCCTGAGCTTCTCTGGTGGCTTGACGCTTCCCTGGCT 556

RESULT 14
BJ004361/c
LOCUS   BJ004361 MFO1SSA cDNA Oryzias latipes cDNA clone MFO1SSA064D03 5',
DEFINITION mRNA sequence.
ACCESSION BJ004361
VERSION   BJ004361.1 GI:17355872
KEYWORDS EST.
SOURCE    Oryzias latipes (Japanese medaka)
ORGANISM Oryzias latipes
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
          Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
          Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
REFERENCE
AUTHORS  1 (bases 1 to 495)
          Kohara, Y., Shin-i, T., Kimura, T., Narita, T., Jindo, T. and Takeda, H.
          Medaka EST Project in Takeda's lab
          Unpublished (2001)
          Contact: Tadasu Shin-i
          Center For Genetic Resource Information
          National Institute of Genetics
          1111 Yata, Mishima, Shizuoka 411-8540, Japan
          Tel: 81-559-81-6856

```

Fax: 81-559-81-6855

Email: tshini@genes.nig.ac.jp.

FEATURES

source

1. 495
Location/Qualifiers
/organism="Oryzias latipes"
/mol_type="mRNA"
/strain="Hd-rr"
/db_xref="taxon:8090"
/clone="MF01SSA064D03"
/sex="mixture of female and male"
/tissue_type="whole embryo"
/dev_stage="segmentation stage 20 - 25"
/clone_lib="MF01SSA cDNA"

ORIGIN

Query Match 51.6%; Score 29.4; DB 12; Length 495;
Best Local Similarity 47.1%; Pred. No. 4.8e+03;
Matches 24; Conservative 14; Mismatches 13; Indels 0; Gaps 0;

QY 4 UCCACCUCUCGCGGNNNDNUGGCAUGGCGCUUCGCAUGGCUAAGGA 54
Db 85 TCCAGCTCCTCTCGTCAGTGGGTGCGTTTCGTGTCGCGAGTGGA 35

RESULT 15

BE386169/c

LOCUS

DEFINITION 60127441F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3615363 5',
mRNA sequence.

ACCESSION

BE386169

VERSION

BE386169.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 513)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC/DCTP/DTP

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

Plate: LLCM279 row: f column: 04

High quality sequence start: 15

High quality sequence stop: 513.

Location/Qualifiers

1. 513

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/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:3615363"

/tissue_type="melanotic melanoma"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH MGC_20"

/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:

EcoRI; cDNA made by oligo-dT priming. Directionally

cloned into EcoRI/XhoI sites using the following 5'

adaptor: GGCACGAG(G). Size-selected >500bp for average

insert size 1.8kb. Library constructed by Ling Hong in

the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 51.6%; Score 29.4; DB 10; Length 513;
Best Local Similarity 49.0%; Pred. No. 4.9e+03;
Matches 25; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

QY 1 GGGUCCACCUCUCGCGGNNNDNUGGCAUGGCGCUUCGCAUGGCUAAG 51
Db 58 GGGTGCTCCTCTCGGACCTTGTCTGCTCATGGCGCTGCGGTGAAGAG 8

Search completed: May 19, 2004, 04:51:37
Job time : 3251 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model
Run on: May 19, 2004, 01:34:20 ; Search time 403 Seconds
(without alignments)
600.862 Million cell updates/sec

Title: RIBOZYME1A
Perfect score: 57
Sequence: 1 ggguccaccuccgcgcggun.....ucscgauggcuaggagcccc 57

Scoring table: IDENTITY NUCDX
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04.*
1: Geneseqn1980s.*
2: Geneseqn1990s.*
3: Geneseqn2000s.*
4: Geneseqn2001as.*
5: Geneseqn2001bs.*
6: Geneseqn2002s.*
7: Geneseqn2003as.*
8: Geneseqn2003bs.*
9: Geneseqn2003cs.*
10: Geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56.2	98.6	57	3 AAZ57636	Aaz57636 Trans-act
2	56.2	98.6	57	3 AAZ57637	Aaz57637 Trans-act
3	46.6	81.8	57	3 AAZ57638	Aaz57638 Trans-act
4	34.6	60.7	37	3 AAZ57639	Aaz57639 Nucleotid
5	31	54.4	61	2 AAQ46667	Aaq46667 Substrate
6	29.6	51.9	51	2 AAQ86173	Aaq86173 Primer HD
7	29.6	51.9	52	2 AAQ86204	Aaq86204 Sindbis/H
8	29.6	51.9	52	2 AAT31151	Aat31151 HDV rever
9	29.6	51.9	52	2 AAT30817	Aat30817 HDV riboz
10	29.6	51.9	52	2 AAV42394	Aav42394 Nested PC
11	29.6	51.9	52	2 AAV42426	Aav42426 Forward P
12	29.6	51.9	52	2 AAV60154	Aav60154 Nested PC
13	29.6	51.9	52	2 AAV60185	Aav60185 Reverse P
14	29.6	51.9	52	2 AAV70746	Aav70746 Reverse P
15	29.6	51.9	52	2 AAV70714	Aav70714 Nested pr
16	29.6	51.9	52	3 AAZ292930	Aaz292930 Hepatitis
17	29.6	51.9	52	3 AAZ292970	Aaz292970 Hepatitis
18	29.6	51.9	52	3 AAZ292843	Aaz292843 Hepatitis
19	29.6	51.9	52	3 AAZ292803	Aaz292803 Hepatitis
20	29.6	51.9	52	6 AAL38850	Aal38850 Alphaviru
21	29.6	51.9	52	6 AAL38810	Aal38810 Alphaviru
22	29.6	51.9	52	6 ABK46276	Abk46276 HDV antig
23	29.6	51.9	52	6 ABK46316	Abk46316 Hepatitis

24	29.6	51.9	80	2 AAZ53138	Aaz53138 Substrate
25	29.6	51.9	80	2 AAZ53140	Aaz53140 Substrate
26	29.6	51.9	83	5 AAF28121	Aaf28121 HDV riboz
27	29.6	51.9	85	2 AAQ46665	Aaq46665 Self-clea
28	29.6	51.9	86	2 AAQ46663	Aaq46663 Self-clea
29	29.6	51.9	90	2 AAX76586	Aax76586 Hepatitis
30	29.6	51.9	90	5 AAF84035	Aaf84035 EPO gene
c 31	29.6	51.9	90	5 AAF84036	Aaf84036 EPO gene
32	29.6	51.9	91	7 ABZ82120	Abz82120 Hepatitis
c 33	29.6	51.9	99	7 ABZ82121	Abz82121 Hepatitis
34	29.6	51.9	567	1 AAN82174	Aan82174 Clone del
c 35	29.6	51.9	1679	1 AAN82172	Aan82172 cDNA corr
c 36	29.6	51.9	1688	7 ABZ77701	Abz77701 Nucleotid
37	29.6	51.9	5451	8 ADA41729	Ada41729 Plasmid p
38	29.6	51.9	8085	9 ADE48122	Ade48122 DNA HCV r
39	29.6	51.9	8100	2 AAX76588	Aax76588 SFV Ecorv
40	29.6	51.9	8732	9 ADE48121	Ade48121 RNA HCV r
41	29.6	51.9	12474	2 AAX78131	Aax78131 Plasmid p
42	29.6	51.9	14311	2 AAT38744	Aat38744 Plasmid p
c 43	29.6	51.9	14311	5 AAF28116	Aaf28116 Vesicular
44	29.6	51.9	14311	5 AAF28115	Aaf28115 Vesicular
45	29.6	51.9	15538	2 AAX76582	Aax76582 Plasmid p

ALIGNMENTS

RESULT 1
AAZ57636
ID AAZ57636 standard; RNA; 57 BP.
XX
AC AAZ57636;
XX
DT 05-APR-2000 (first entry)
XX
DE Trans-acting antigenomic delta ribozyme, deltaRzPl.1 nucleotide sequence.
XX
KW Trans-acting antigenomic delta ribozyme; viral RNA cleavage;
XX
KW inherited disease; deltaRzPl.1; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_binding 1..6
FT /tag= a
FT /note= "Forms double stranded region with bases 52-57"
FT stem_loop 7..19
FT /tag= b
FT misc_binding 20..25
FT /tag= c
FT /bound moiety= "SP1.1 substrate (AAZ57641) bases 5-11"
FT stem_loop 30..45
FT /tag= d
FT misc_binding 52..57
FT /tag= e
FT /note= "Forms a double stranded region with bases 6-1"
XX WO9955856-A2.
PD 04-NOV-1999.
XX
XX 29-APR-1999; 99WO-CA000391.
XX
XX 29-APR-1998; 98CA-02230203.
XX (UYSH) UNIV SHERBROOKE.
XX
XX Perreault J, Ananvoranich S, Lafontaine D;
XX WPI; 2000-096791/08.
XX
XX New construction of nucleic acid enzyme useful for biotechnological,
FT diagnostic and therapeutic applications.

FT /*tag= g
 FT /note= "RNA substrate binding region"
 FT misc_structure 33. .37
 FT /*tag= i
 FT /label= stem_IV
 FT /note= "forms duplex with region 42. .45"
 FT stem_loop 34. .45
 FT /*tag= h
 FT misc_feature 42. .45
 FT /*tag= j
 FT /label= stem_IV
 FT /note= "forms duplex with region 33. .37"
 FT misc_feature 52. .55
 FT /*tag= c
 FT /label= stem_II
 FT /note= "forms duplex with region 7. .10"

XX WO9314218-A1.

XX PN

XX PD

XX PF 12-JAN-1993; 93WO-US000292.

XX PR 13-JAN-1992; 92US-00821155.

XX PA (UYDU-) UNIV DUKE.

XX PI Been MD, Rosenstein SP, Perrota AT;

XX DR WPI; 1993-243233/30.

XX Nucleic acid molecule having RNA substrate-cleaving enzymatic activity -
 useful for cleaving specific target molecules in-vitro.

XX PS Disclosure; Fig 8; 55pp; English.

XX The self-cleaving sequences from genomic and antigenomic HDV can be used
 to develop enzymatic RNA mols. with similar properties. ADC3 is a smaller
 version of ADC1 (AAQ53138), wherein stem IV is shortened. Such a smaller
 enzymatic RNA has simplified synthesis and the potential for higher
 specific activity due to a higher probability that a small RNA will fold
 into an enzymatically active structure. (Updated on 25-MAR-2003 to
 correct PN field.)

XX SQ Sequence 61 BP; 10 A; 20 C; 19 G; 0 T; 12 U; 0 Other;

Query Match 54.4%; Score 31; DB 2; Length 61;
 Best Local Similarity 77.4%; Pred. No. 16;
 Matches 41; Conservative 6; Mismatches 2; Indels 4; Gaps 1;

QY 4 UCCACCUCCGCGGUNNNDNNGGCAUGCGGCUUGGCUAAGGACC 56

Db 8 UCCACCUCCGCGGUCGACCGGCAU---CUUCGGAUGGCUAAGGAGC 56

RESULT 6

AAQ86173

ID AAQ86173 standard; DNA; 51 BP.

AC AAQ86173;

DT 25-MAR-2003 (revised)

DT 21-NOV-1995 (first entry)

XX Primer HDV17-68 amplifies vector DNA to initiate Sindbis infection.

XX Eukaryotic layered vector initiation system; Sindbis; alphavirus; PCR;
 transcriptions initiation; non-structural protein; subgenomic fragment;
 RNA polymerase recognition sequence; ELVIS; gene therapy; amplify;
 primer; polymerase chain reaction; cystic fibrosis; ss.

XX Synthetic.

XX OS

PN WO9507994-A2.
 XX 23-MAR-1995.
 XX PF 15-SEP-1994; 94WO-US010469.
 XX PR 15-SEP-1993; 93US-00122791.
 XX PR 18-FEB-1994; 94US-00198450.
 XX PA (VIAG-) VIAGENE INC.
 XX Dubensky TW, Ibanez CE, Chang SM, Jolly DJ, Driver DA, Polo JM;
 WPI; 1995-131362/17.
 XX New alpha virus vectors for gene therapy - of viral infection, cancer,
 auto-immune disease, etc., and as vaccines.
 XX Example 2; Page 68; 260pp; English.

XX The sequences given in AAQ86167-81 are primers which were used in the
 generation of plasmid DNA which initiates Sindbis infection. The
 amplified DNA sequences were used in the construction of a eukaryotic
 layered vector initiation system (ELVIS) derived from Sindbis. ELVIS's
 comprise a 5' sequence capable of initiating transcription of an
 alphavirus, a nucleotide sequence encoding alphavirus non-structural
 proteins, a viral junction region which has been inactivated such that
 viral transcription of the subgenomic fragment is prevented, and an
 alphavirus RNA polymerase recognition sequence. Inactivation of the viral
 junction region prevents transcription of the subgenomic fragment making
 vectors such as this suitable for a wide variety of applications, eg.
 gene therapy for the treatment of cystic fibrosis. (Updated on 25-MAR-
 2003 to correct PN field.)

XX SQ Sequence 51 BP; 9 A; 20 C; 14 G; 8 T; 0 U; 0 Other;

Query Match 51.9%; Score 29.6; DB 2; Length 51;
 Best Local Similarity 59.4%; Pred. No. 43;
 Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCCGCGGUNNNDNNGGCAUGCG 35

Db 1 TCCACCTCTCGCGTCCGACCTCGCATCCG 32

RESULT 7

AAQ86204

ID AAQ86204 standard; DNA; 52 BP.

AC AAQ86204;

DT 25-MAR-2003 (revised)

DT 23-NOV-1995 (first entry)

XX Sindbis/HDV ribozyme sequence reverse primer, HDV17-68.

XX Eukaryotic layered vector initiation system; Sindbis; alphavirus; PCR;
 transcriptions initiation; non-structural protein; subgenomic fragment;
 RNA polymerase recognition sequence; ELVIS; gene therapy; amplify;
 primer; polymerase chain reaction; cystic fibrosis; ss.

XX Synthetic.

XX WO9507994-A2.

XX 23-MAR-1995.

XX 15-SEP-1994; 94WO-US010469.

XX 15-SEP-1993; 93US-00122791.

XX 18-FEB-1994; 94US-00198450.

XX (VIAG-) VIAGENE INC.

XX PI Dubensky TW, Ibanez CE, Chang SM, Jolly DJ, Driver DA, Polo JM;
 XX WPI; 1995-131362/17.
 XX
 XX New alpha virus vectors for gene therapy - of viral infection, cancer,
 PT auto-immune disease, etc., and as vaccines.
 XX
 XX Example 7; Page 114; 260pp; English.
 XX
 CC The sequences given in AAO86200-15 are primers which were used in the
 CC production of alphavirus vectors expressing multiple heterologous genes.
 CC These vectors are eukaryotic layered vector initiation systems (ELVIS)
 CC derived from Sindbis. ELVIS's comprise a 5' sequence capable of
 CC initiating transcription of an alphavirus, a nucleotide sequence encoding
 CC alphavirus non-structural proteins, a viral junction region which has
 CC been inactivated such that viral transcription of the subgenomic fragment
 CC is prevented, and an alphavirus RNA polymerase recognition sequence.
 CC Inactivation of the viral junction region prevents transcription of the
 CC subgenomic fragment making vectors such as this suitable for a wide
 CC variety of applications, eg. gene therapy for the treatment of cystic
 CC fibrosis. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 XX Sequence 52 BP; 9 A; 21 C; 14 G; 8 T; 0 U; 0 Other;
 SQ
 Query Match 51.9%; Score 29.6; DB 2; Length 52;
 Best Local Similarity 59.4%; Pred. No. 43;
 Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;
 QY 4 UCCACCUCCUGCGGCGGCTCCGACCTGGGCATCCG 35
 Db 1 TCCACCTCTCGCGGCTCCGACCTGGGCATCCG 32
 RESULT 8
 AAT31151
 ID AAT31151 standard; DNA; 52 BP.
 XX
 AC AAT31151;
 XX
 DT 12-SEP-1996 (first entry)
 XX
 DE HDV reverse primer HDV17-68.
 XX
 XX Alphavirus; Sindbis virus; vector; gene therapy; vaccine;
 KW polymerase chain reaction; PCR; primer; hepatitis delta virus; HDV;
 KW ribozyme; ss.
 XX
 OS Synthetic.
 XX
 PN WO9617072-A2.
 XX
 PD 06-JUN-1996.
 XX
 PF 30-NOV-1995; 95WO-US015490.
 XX
 PR 30-NOV-1994; 94US-00348472.
 PR 18-JAN-1995; 95US-00376184.
 PR 15-MAR-1995; 95US-00405827.
 XX
 PA (CHIR) CHIRON VIAGENE INC.
 XX
 XX Dubensky TW, Polo JM, Ibanez CE, Chang SMW, Jolly DJ, Driver DA;
 PI Belli BA;
 PI
 XX
 DR WPI; 1996-277785/28.
 XX
 XX New recombinant alpha-virus vectors - used to develop prods and methods
 PT for use in gene therapy and in the prodn. of vaccines.
 PT
 XX
 PS Example 7; Page 120; 256pp; English.
 XX
 CC Primer HDV17-68 (AAT31151) is based on hepatitis delta virus (HDV)

CC nucleotides 839-887. It was used with reverse primer HDV49-XC (AAT30850)
 CC for the PCR amplification of HDV sequences. A second primer pair, SIN-HDV
 CC (AAT31152) and SIN276-SPE (AAT31153), is used to amplify a fragment
 CC contg. Sindbis 5'-end sequences fused to HDV sequences. Overlapping
 CC synthesis is used in a second round of PCR using primers HDV49-XC and
 CC elements HDV ribozyme/Sindbis 5'-end 299 nts/Sindbis junction
 CC region/Sindbis structural protein genes/Sindbis 3'-end untranslated
 CC line cassettes were constructed that allow inducible expression of
 CC structural proteins via alphavirus vectors
 XX
 XX Sequence 52 BP; 9 A; 21 C; 14 G; 8 T; 0 U; 0 Other;
 SQ
 Query Match 51.9%; Score 29.6; DB 2; Length 52;
 Best Local Similarity 59.4%; Pred. No. 43;
 Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;
 QY 4 UCCACCUCCUGCGGCGGCTCCGACCTGGGCATCCG 35
 Db 1 TCCACCTCTCGCGGCTCCGACCTGGGCATCCG 32
 RESULT 9
 AAT30817
 ID AAT30817 standard; DNA; 52 BP.
 XX
 AC AAT30817;
 XX
 DT 12-SEP-1996 (first entry)
 XX
 DE HDV ribozyme primer HDV17-68.
 XX
 KW Alphavirus; Sindbis virus; vector; gene therapy; vaccine; primer;
 KW polymerase chain reaction; PCR; ELVIS; ribozyme; HDV;
 KW hepatitis delta virus; ss.
 XX
 OS Synthetic.
 XX
 PN WO9617072-A2.
 XX
 PD 06-JUN-1996.
 XX
 PF 30-NOV-1995; 95WO-US015490.
 XX
 PR 30-NOV-1994; 94US-00348472.
 PR 18-JAN-1995; 95US-00376184.
 PR 15-MAR-1995; 95US-00405827.
 XX
 PA (CHIR) CHIRON VIAGENE INC.
 XX
 XX Dubensky TW, Polo JM, Ibanez CE, Chang SMW, Jolly DJ, Driver DA;
 PI Belli BA;
 PI
 XX
 DR WPI; 1996-277785/28.
 XX
 XX New recombinant alpha-virus vectors - used to develop prods and methods
 PT for use in gene therapy and in the prodn. of vaccines.
 PT
 XX
 PS Example 3; Page 85; 256pp; English.
 XX
 XX Primer SHDV1F (AAT30816) contains a buffer sequence allowing enzyme
 CC digestion, a SacI site, and a hepatitis delta virus (HDV) ribozyme
 CC sequence. It was used with nested primer HDV17-68 (AAT30817) and reverse
 CC primer SHDV84R (AAT30818) to generate an HDV ribozyme. This antigenomic
 CC ribozyme can be placed between the polyA tract at the 3' end of a Sindbis
 CC virus-based eukaryotic layered vector initiation system, ELVIS, and the
 CC transcription terminal signals to produce alphavirus expression vectors
 CC useful in methods of gene therapy and for vaccine prodn
 XX
 XX Sequence 52 BP; 9 A; 21 C; 14 G; 8 T; 0 U; 0 Other;
 SQ
 Query Match 51.9%; Score 29.6; DB 2; Length 52;


```

XX PD 29-SEP-1998.
XX PF 30-OCT-1996; 96US-00739158.
XX PR 15-SEP-1993; 93US-00122791.
XX PR 18-FEB-1994; 94US-00198450.
XX PR 14-SEP-1994; 94WO-US010469.
XX PR 30-NOV-1994; 94US-00348472.
XX PR 18-JAN-1995; 95US-00376184.
XX PR 15-MAR-1995; 95US-00404796.
XX PA (POLO/) POLO J M.
XX PA (DUBE/) DUBENSKY T W.
XX PA (JOLLY/) JOLLY D J.
XX PA (DRIV/) DRIVER D A.
XX PI Driver DA, Polo JM, Jolly DJ, Dubensky TW;
XX WPI; 1998-541753/46.
XX Eukaryotic layered vector initiation system - containing eukaryotic
XX promoter and heterologous antigen coding sequence, useful for stimulating
XX immune response.
XX Example 3; Col 71-72; 144pp; English.
XX PCR primers AAV60153-55 are used to amplify Hepatitis delta virus
XX ribozyme sequence. The product is used in the course of the invention.
XX The specification describes an eukaryotic layered vector initiation
XX system, based on Sindbis. The eukaryotic layered vector initiation
XX system comprises a eukaryotic promoter 5' of viral cDNA which initiates, in a
XX susceptible target cell, 5' to 3' synthesis of RNA from the viral cDNA.
XX The RNA comprises a vector construct which autonomously amplifies in the
XX cell and expresses a heterologous nucleic acid sequence which encodes an
XX antigen or modified form that stimulates an immune response within an
XX animal. The system is useful for stimulating an immune response to an
XX antigen by introducing the vector into target cells, preferably by
XX infection in vivo, especially where the immune response is a cell
XX mediated, HLA class I-restricted or an HLA class II-restricted immune
XX response. (Updated on 25-MAR-2003 to correct PR field.)
XX SQ Sequence 52 BP; 9 A; 21 C; 14 G; 8 T; 0 U; 0 Other;
Query Match 51.9%; Score 29.6; DB 2; Length 52;
Best Local Similarity 59.4%; Pred. No. 43;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;
Qy 4 UCCACCUCUCGCGGUNNNNNUGGCGAUGCG 35
Db 1 TCCACCTCCTCGCGTCCGACCTGGCATCCG 32
RESULT 13
AAV60185
ID AAV60185 standard; DNA; 52 BP.
AC AAV60185;
XX 25-MAR-2003 (revised)
DT 04-DEC-1998 (first entry)
XX Reverse PCR primer HDV17-68.
XX Eukaryotic layered vector initiation system; stimulate; immune response;
XX Sindbis; PCR primer; ss.
XX Synthetic.
XX US5814482-A.
XX 29-SEP-1998.
XX

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PF 30-OCT-1996; 96US-00739158.
XX 15-SEP-1993; 93US-00122791.
XX PR 18-FEB-1994; 94US-00198450.
XX PR 14-SEP-1994; 94WO-US010469.
XX PR 30-NOV-1994; 94US-00348472.
XX PR 18-JAN-1995; 95US-00376184.
XX PR 15-MAR-1995; 95US-00404796.
XX PA (POLO/) POLO J M.
XX PA (DUBE/) DUBENSKY T W.
XX PA (JOLLY/) JOLLY D J.
XX PA (DRIV/) DRIVER D A.
XX PI Driver DA, Polo JM, Jolly DJ, Dubensky TW;
XX WPI; 1998-541753/46.
XX Eukaryotic layered vector initiation system - containing eukaryotic
XX promoter and heterologous antigen coding sequence, useful for stimulating
XX immune response.
XX Example 5; Col 108; 144pp; English.
XX PCR primers AAV60184-85 are used in the course of the invention. The
XX specification describes an eukaryotic layered vector initiation system,
XX based on Sindbis. The eukaryotic layered vector initiation system
XX comprises a eukaryotic promoter 5' of viral cDNA which initiates, in a
XX susceptible target cell, 5' to 3' synthesis of RNA from the viral cDNA.
XX The RNA comprises a vector construct which autonomously amplifies in the
XX cell and expresses a heterologous nucleic acid sequence which encodes an
XX antigen or modified form that stimulates an immune response within an
XX animal. The system is useful for stimulating an immune response to an
XX antigen by introducing the vector into target cells, preferably by
XX infection in vivo, especially where the immune response is a cell
XX mediated, HLA class I-restricted or an HLA class II-restricted immune
XX response. (Updated on 25-MAR-2003 to correct PR field.)
XX SQ Sequence 52 BP; 9 A; 21 C; 14 G; 8 T; 0 U; 0 Other;
Query Match 51.9%; Score 29.6; DB 2; Length 52;
Best Local Similarity 59.4%; Pred. No. 43;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;
Qy 4 UCCACCUCUCGCGGUNNNNNUGGCGAUGCG 35
Db 1 TCCACCTCCTCGCGTCCGACCTGGCATCCG 32
RESULT 14
AAV70746
ID AAV70746 standard; DNA; 52 BP.
AC AAV70746;
XX 20-MAR-2003 (revised)
DT 02-FEB-1999 (first entry)
XX Reverse PCR primer HDV17-68 used to amplify Hepatitis delta virus.
XX Alphavirus vector construct; gene therapy; PCR primer; ss.
XX Synthetic.
XX Hepatitis D virus.
XX US5843723-A.
XX 01-DEC-1998.
XX 30-OCT-1996; 96US-00739167.
XX 15-SEP-1993; 93US-00122791.
XX PR 18-FEB-1994; 94US-00198450.

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PR 30-NOV-1994; 94US-00348472.
PR 20-JAN-1995; 95US-00376184.
PR 15-MAR-1995; 95US-00404796.
PA (CHIR ) CHIRON CORP.
XX
PI Chang SMW, Jolly DJ, Dubensky TW, Belli BA, Ibanez CE, Driver DA;
PI Polo JW;
XX
XX WPI; 1999-044581/04.
XX
XX Alphavirus vectors constructs containing a 5' promoter of viral cDNA by
PT in vitro transcription - used in gene therapy.
XX
XX Example 7; Col 103; 140pp; English.
XX
XX PCR primers AAV70745-46 are used to amplify part of the hepatitis delta
CC virus (HDV) genome. The amplified product is used in the production of
CC the alphavirus vector constructs of the invention. These constructs
CC comprise a promoter 5' of viral cDNA which initiates the synthesis of RNA
CC from the viral cDNA by in vitro transcription, followed by a 5' sequence
CC which initiates transcription of alphavirus RNA, followed by a nucleotide
CC sequence encoding alphavirus nonstructural proteins, a viral junction
CC region which has been inactivated such that viral transcription of a
CC subgenomic fragment is prevented, an internal ribosome entry site or a
CC sequence which promotes ribosome read through between adjacent reading
CC frames, and an alphavirus RNA polymerase recognition sequence. The
CC recombinant alphavirus vectors can be used for gene therapy. (Updated on
CC 20-MAR-2003 to correct PR field.)
XX
SQ Sequence 52 BP; 9 A; 21 C; 14 G; 8 T; 0 U; 0 Other;

Query Match 51.9%; Score 29.6; DB 2; Length 52;
Best Local Similarity 59.4%; Pred. No. 43;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCCUGCGGUNNNDNNUGGGCAUGCG 35
Db 1 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 32

RESULT 15
AAV70714
ID AAV70714 standard; DNA; 52 BP.
XX
AC AAV70714;
XX
XX 20-MAR-2003 (revised)
DT 02-FEB-1999 (first entry)
XX
XX Nested primer HDV17-68 for hepatitis delta virus ribozyme sequence.
XX
XX Alphavirus vector construct; gene therapy; PCR primer; ss.
XX
XX Synthetic.
OS Hepatitis D virus.
XX
XX US5843723-A.
XX
XX 01-DEC-1998.
XX
XX 30-OCT-1996; 96US-00739167.
XX
XX 15-SEP-1993; 93US-00122791.
PR 18-FEB-1994; 94US-00198450.
PR 30-NOV-1994; 94US-00348472.
PR 20-JAN-1995; 95US-00376184.
PR 15-MAR-1995; 95US-00404796.
XX
XX (CHIR ) CHIRON CORP.
XX
XX Chang SMW, Jolly DJ, Dubensky TW, Belli BA, Ibanez CE, Driver DA;
PI Polo JW;

```

```

XX WPI; 1999-044581/04.
XX
XX Alphavirus vectors constructs containing a 5' promoter of viral cDNA by
PT in vitro transcription - used in gene therapy.
XX
XX Example 3; Col 69; 140pp; English.
XX
XX PCR primers AAV70713-15 are overlapping primers used to amplify hepatitis
CC delta virus (HDV) ribozyme sequences. The amplified product is used in
CC the production of the alphavirus vector constructs of the invention.
CC These constructs comprise a promoter 5' of viral cDNA which initiates the
CC synthesis of RNA from the viral cDNA by in vitro transcription, followed
CC by a 5' sequence which initiates transcription of alphavirus RNA,
CC followed by a nucleotide sequence encoding alphavirus nonstructural
CC proteins, a viral junction region which has been inactivated such that
CC viral transcription of a subgenomic fragment is prevented, an internal
CC ribosome entry site or a sequence which promotes ribosome read through
CC between adjacent reading frames, and an alphavirus RNA polymerase
CC recognition sequence. The recombinant alphavirus vectors can be used for
CC gene therapy. (Updated on 20-MAR-2003 to correct PR field.)
XX
SQ Sequence 52 BP; 9 A; 21 C; 14 G; 8 T; 0 U; 0 Other;

Query Match 51.9%; Score 29.6; DB 2; Length 52;
Best Local Similarity 59.4%; Pred. No. 43;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCCUGCGGUNNNDNNUGGGCAUGCG 35
Db 1 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 32

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Pred. No. is the number of results predicted by chance to have a

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and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
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3	56.2	98.6	57	6	AX012286	AX012286 Sequence
4	56.2	98.6	57	6	AX012287	AX012287 Sequence
5	56.2	98.6	57	6	AX012288	AX012288 Sequence
6	56.2	98.6	57	6	AX012289	AX012289 Sequence
7	56.2	98.6	57	6	AX012290	AX012290 Sequence
8	55.4	97.2	57	6	AX012285	AX012285 Sequence
9	46.6	81.8	57	6	AX012284	AX012284 Sequence
10	36.2	63.5	37	6	AX012291	AX012291 Sequence
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C 12	31	54.4	61	6	141390	141390 Sequence 18
C 13	29.8	52.3	159423	9	AC008429	AC008429 Homo sapi
C 14	29.8	52.3	171914	2	AC119266	AC119266 Mus muscu
C 15	29.8	52.3	184032	2	AC117632	AC117632 Mus muscu
C 16	29.8	52.3	213025	2	AC021159	AC021159 Homo sapi
C 17	29.6	51.9	52	6	AR021007	AR021007 Sequence
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C 19	29.6	51.9	52	6	AR043422	AR043422 Sequence
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C 21	29.6	51.9	52	6	AR062337	AR062337 Sequence
C 22	29.6	51.9	52	6	AR062377	AR062377 Sequence
C 23	29.6	51.9	52	6	AR183796	AR183796 Sequence
C 24	29.6	51.9	52	6	AR183836	AR183836 Sequence
C 25	29.6	51.9	52	6	AR368179	AR368179 Sequence
C 26	29.6	51.9	52	6	AR368219	AR368219 Sequence
C 27	29.6	51.9	80	6	141388	141388 Sequence 16
C 28	29.6	51.9	83	6	AR123021	AR123021 Sequence
C 29	29.6	51.9	84	6	141385	141385 Sequence 13
C 30	29.6	51.9	84	6	141386	141386 Sequence 14
C 31	29.6	51.9	86	6	141378	141378 Sequence 6
C 32	29.6	51.9	90	6	AR243300	AR243300 Sequence
C 33	29.6	51.9	90	6	AR342596	AR342596 Sequence
C 34	29.6	51.9	90	6	AR342597	AR342597 Sequence
C 35	29.6	51.9	90	6	AX174838	AX174838 Sequence
C 36	29.6	51.9	90	6	AX174839	AX174839 Sequence
C 37	29.6	51.9	90	6	BD226817	BD226817 Alphaviru
C 38	29.6	51.9	101	6	AR363756	AR363756 Sequence 11
C 39	29.6	51.9	105	6	141844	141844 Sequence 25
C 40	29.6	51.9	105	6	141849	141849 Sequence 30
C 41	29.6	51.9	567	6	105156	105156 Sequence 11
C 42	29.6	51.9	866	14	HPDJS1	D90192 Hepatitis D
C 43	29.6	51.9	866	14	HPDJS2	D90193 Hepatitis D
C 44	29.6	51.9	868	14	HPDJM1	D90190 Hepatitis D
C 45	29.6	51.9	868	14	HPDJM2	D90191 Hepatitis D

ALIGNMENTS

RESULT 1	AX012282	Sequence 44 from Patent WO9955856.	57 bp	RNA	linear	PAT 06-SEP-2000
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DEFINITION	Sequence 44 from Patent WO9955856.					
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VERSION	AX012282.1	GI:9998343				
KEYWORDS	synthetic construct					
SOURCE	synthetic construct					
ORGANISM	artificial sequences.					
REFERENCE	1					
AUTHORS	Ananvoranich, S., Lafontaine, D. and Perreault, J.P.					
TITLE	Nucleic acid enzyme for rna cleavage					
JOURNAL	Patent: WO 9955856-A 44 04-NOV-1999;					
	ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN					

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FEATURES
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    PIERRE (CA); UNIV SHERBROOKE (CA)
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RESULT 2
LOCUS AX012283 57 bp RNA linear PAT 06-SEP-2000
DEFINITION Sequence 45 from Patent WO9955856.
ACCESSION AX012283
VERSION AX012283.1 GI:9998344
KEYWORDS
SOURCE
  ORGANISM
    synthetic construct
    artificial sequences.
REFERENCE
  1
  AUTHORS
    Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
  TITLE
    Nucleic acid enzyme for rna cleavage
  JOURNAL
    Patent: WO 9955856-A 45 04-NOV-1999;
    ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
    PIERRE (CA); UNIV SHERBROOKE (CA)
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  Best Local Similarity 71.9%; Pred. No. 1.3e-05;
  Matches 41; Conservative 16; Mismatches 0; Indels 0; Gaps 0;

  Qy 1 GGGUCCACCUCCUGCGGUNNNDNUGGCAUGGCGGUUCGCAUGGCUAAGGGACCC 57
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
  Db 1 GGGTCCACCTCTCGCGTCCGACCTGGGCATGGGCTTCGCATGGCTAAGGGACCC 57

RESULT 3
LOCUS AX012286 57 bp RNA linear PAT 06-SEP-2000
DEFINITION Sequence 48 from Patent WO9955856.
ACCESSION AX012286
VERSION AX012286.1 GI:9998347
KEYWORDS
SOURCE
  ORGANISM
    synthetic construct
    artificial sequences.
REFERENCE
  1
  AUTHORS
    Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
  TITLE
    Nucleic acid enzyme for rna cleavage
  JOURNAL
    Patent: WO 9955856-A 48 04-NOV-1999;
    ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
    PIERRE (CA); UNIV SHERBROOKE (CA)
FEATURES
  source
    1..57
    /organism="synthetic construct"
    /mol_type="unassigned RNA"
    /db_xref="taxon:32630"
    /note="synthetic nucleic acid"
ORIGIN
  Query Match      98.6%; Score 56.2; DB 6; Length 57;
  Best Local Similarity 71.9%; Pred. No. 1.3e-05;
  Matches 41; Conservative 16; Mismatches 0; Indels 0; Gaps 0;

  Qy 1 GGGUCCACCUCCUGCGGUNNNDNUGGCAUGGCGGUUCGCAUGGCUAAGGGACCC 57
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
  Db 1 GGGTCCACCTCTCGCGTCCGACCTGGGCATGGGCTTCGCATGGCTAAGGGACCC 57

RESULT 4
LOCUS AX012287 57 bp RNA linear PAT 06-SEP-2000
DEFINITION Sequence 49 from Patent WO9955856.
ACCESSION AX012287
VERSION AX012287.1 GI:9998348
KEYWORDS
SOURCE
  ORGANISM
    synthetic construct
    artificial sequences.
REFERENCE
  1
  AUTHORS
    Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
  TITLE
    Nucleic acid enzyme for rna cleavage
  JOURNAL
    Patent: WO 9955856-A 49 04-NOV-1999;
    ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
    PIERRE (CA); UNIV SHERBROOKE (CA)
FEATURES
  source
    1..57
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    /note="synthetic nucleic acid"
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  Query Match      98.6%; Score 56.2; DB 6; Length 57;
  Best Local Similarity 71.9%; Pred. No. 1.3e-05;
  Matches 41; Conservative 16; Mismatches 0; Indels 0; Gaps 0;

  Qy 1 GGGUCCACCUCCUGCGGUNNNDNUGGCAUGGCGGUUCGCAUGGCUAAGGGACCC 57
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  Db 1 GGGTCCACCTCTCGCGTCCGACCTGGGCATGGGCTTCGCATGGCTAAGGGACCC 57

RESULT 5
LOCUS AX012288 57 bp RNA linear PAT 06-SEP-2000
DEFINITION Sequence 50 from Patent WO9955856.
ACCESSION AX012288
VERSION AX012288.1 GI:9998349
KEYWORDS
SOURCE
  ORGANISM
    synthetic construct
    artificial sequences.
REFERENCE
  1
  AUTHORS
    Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
  TITLE
    Nucleic acid enzyme for rna cleavage
  JOURNAL
    Patent: WO 9955856-A 50 04-NOV-1999;
    ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
    PIERRE (CA); UNIV SHERBROOKE (CA)
FEATURES
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    1..57
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    /mol_type="unassigned RNA"
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    /note="synthetic nucleic acid"
ORIGIN
  Query Match      98.6%; Score 56.2; DB 6; Length 57;
  Best Local Similarity 71.9%; Pred. No. 1.3e-05;
  Matches 41; Conservative 16; Mismatches 0; Indels 0; Gaps 0;

  Qy 1 GGGUCCACCUCCUGCGGUNNNDNUGGCAUGGCGGUUCGCAUGGCUAAGGGACCC 57
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
  Db 1 GGGTCCACCTCTCGCGTCCGACCTGGGCATGGGCTTCGCATGGCTAAGGGACCC 57

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REFERENCE
AUTHORS 1 Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
TITLE Nucleic acid enzyme for rna cleavage
JOURNAL Patent: WO 9955856-A 53 04-NOV-1999;
ANANVORANICH SIRINAT (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
FEATURES
source Location/Qualifiers
1.37
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="synthetic nucleic acid"
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Query Match 63.5%; Score 36.2; DB 6; Length 37;
Best Local Similarity 67.6%; Pred.No.21;
Matches 25; Conservative 12; Mismatches 0; Indels 0; Gaps 0;
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Db 1 GGGTCCACTCTCGCGGTCCGACCTGGCGATCGGC 37
RESULT 11
LOCUS HSA287B20 168545 bp DNA linear PRI 11-MAR-2001
DEFINITION Human DNA sequence from clone RP11-287B20 on chromosome 20 Contains
part of gene KIAA1272 for a protein similar to rat Tulip 2, ESTs,
STSs and GSSs, complete sequence.
ACCESSION AL121896
VERSION AL121896.11 GI:12583641
KEYWORDS HTG; KIAA1272; Tulip.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS 1 (bases 1 to 168545)
TITLE Direct Submision
JOURNAL Submitted (08-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
On Jan 27, 2001 this sequence version replaced gi.8218066.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em., ENBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/projects/C_elegans/wormpep
This sequence
was generated from part of bacterial clone contigs of human
chromosome 20, constructed by the Sanger Centre Chromosome 20
Mapping Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr20
RP11-287B20 is from the library RPI1-11.1 constructed by the group
of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
IMPORTANT: This sequence is not the entire insert of clone
RP11-287B20 It may be shorter because we sequence overlapping
sections only once, except for a 100 base overlap.
The true left end of clone RP11-287B20 is at 1 in this sequence.
The true left end of clone RPS-1049G11 is at 168446 in this
sequence. The true right end of clone RP11-470C13 is at 111612 in
this sequence. This sequence was finished as follows unless
otherwise noted: all regions were either double-stranded or
sequenced with an alternate chemistry or covered by high quality
data (i.e., phred quality >= 30); an attempt was made to resolve
all sequencing problems, such as compressions and repeats; all

```

```

regions were covered by at least one plasmid subclone or more than
one M13 subclone; and the assembly was confirmed by restriction
digest.
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/db_xref="taxon:9606"
/chromosome="20"
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/clone_lib="RPI1-11.1"
23..649
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30..496
/note="L1MB8 repeat: matches 5689..6167 of consensus"
complement(358..678)
/note="match: STS: Em:G25753 Em:G27399"
2049..2584
/note="L2 repeat: matches 2101..2670 of consensus"
5422..5607
/note="WERSB repeat: matches 1..178 of consensus"
5931..6206
/note="Aluub repeat: matches 1..275 of consensus"
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match: GSS: Em:AQ345124"
9283..9746
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complement(9548..10038)
/note="match: GSS: Em:AQ772919"
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/note="match: GSS: Em:AQ409384"
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111814..112585,120218..120401,123707..123844,
124131..124199,125553..125663,130988..131096,
135046..135104,135957..136085,146005..146133))
/gene="bA287B20.1"
/note="continued from dJ1049G11 (AL078634)
match: cDNAs: Em:AK002211 Em:AB032400 Em:AF041106
Em:AF041107 Em:AL050050 Em:AB033098
match: ESTs: Em:T90823 Em:BE467241 Em:BE349987 Em:BE219600
Em:R05337 Em:T85728 Em:AW753998 Em:AW604552 Em:AW658646
Em:R05338
match: proteins: Tr:Q9Y408"
/codon_start=1
/evidence=not experimental
/product="bA287B20.1.1 (KIAA1272 similar to rat tulip
proteins 1 and 2, isoform 1)"
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/db_xref="SPTREMBL:O9B0T6"
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SYWKLQMFETSLPRKMAELIVATFLLPSAEYSVETDKKFIVSLCLLDCMCL
PVSLLHPVSTAVLEQHSARAPLLDIYIRVLHCCVCGSSTYQQSHYILTLADLSST
DYDPLPLANVKSEPVQYHSSAGNLLTVEEEKRSLELIPLTARMVNAHLVNLH
GHVPLSGPAILTHSLVSEHNDNAHVEGSELSEFVFRSPNLQLFVNDSTLLSYLQTP
EGPVGSGPVSLSVVRVIRDISKYSWDGKVLXGPLEGLAPNRPSPFLISWHRD
TFGPKQSSQVEGDDVLDLLENIGHTSPCLLPSPQLNLEPSPFPCRLLDLGMNSWR
TEVILRQAQDEYDIQSHNFDNFMKVTSQQQSPVPRGPFYFCLLDLGMNSWR
RKNPHLLKNSKLRLKLRKQCRTHKIAFYIAEGQDKGSIILSNRSGSADSLT
FVAGLGHVSLDTHCGFMGGLQRNSTGTQYATVSTVIVHVSFRMPSPSDSLT
KKRLHGNDEVHIVWSHSDRYRRGIIPAFGDVSIILYPMKNHMFITAIKKPEVPF
FGPLFDGNIYVSLVCATCINASRAVKCLIPLQSFVEERALIIEALIQNHREV
MTFEDPAQVPSPSPSVLSGT"
11547..12050
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misc_feature

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12786..12980
/note="MER3 repeat: matches 4. .209 of consensus"
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14926..15041
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15330..15369
/note="MIR repeat: matches 106. .148 of consensus"
repeat_region
15335..15474
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17900..18040
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18042..18340
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19137..19367
/note="L2 repeat: matches 2515. .2748 of consensus"
repeat_region
20304..20689
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20690..21000
/note="AluSp repeat: matches 1. .312 of consensus"
repeat_region
21001..21605
/note="LIMB7 repeat: matches 5577. .6169 of consensus"
repeat_region
21618..21881
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22065..22161
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23992..24102
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26203..26306
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29293..29412
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30933..31124
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33955..34242
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36573..37174
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37353..37774
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repeat_region
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Finishing Completed at Stanford Human Genome Center
www.shgc.stanford.edu

Quality: Phrap Quality >=40 99.9% of Sequence;

Estimated Total Number of Errors is 0.1.

NOTE: Shatter libraries failed to resolve dinucleotide repeat region from 21938 to 21990. Forced join at 21980.

FEATURES

source

1. 159423

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/chromosome="5"

/clone="CTC-308K20"

21938..21990

misc_feature

/note="Shatter libraries failed to resolve dinucleotide repeat region from 21938 to 21990. Forced join at 21980."

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Query Match 52.3%; Score 29.8; DB 9; Length 159423;

Best Local Similarity 49.1%; Pred. No. 6.4e+02;

Matches 26; Conservative 13; Mismatches 14; Indels 0; Gaps 0;

Qy 5 CCACUCCUCCGCGGNNNDNNGGCAUGCGGCUUGCAUGGCUAAGGACCC 57

||||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||

Db 17452 CCACCTCTGGCTGATTCAGTCTGGCAAGGGGCTCCCATCATCAGTTGCC 17400

RESULT 14

AC119266

LOCUS

AC119266 171914 bp DNA linear HTG 17-MAR-2003
Mus musculus clone RP24-321G8, WORKING DRAFT SEQUENCE, 11 unordered pieces.

AC119266

AC119266.3 GI:28975955

HTG; HTGS PHASE1; HTGS DRAFT.

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 171914)

Birken, B., Nusbaum, C. and Lander, E.

Mus musculus, clone RP24-321G8

Unpublished

2 (bases 1 to 171914)

Birken, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavskiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campotiano, A., Chang, J., Chazaro, B., Choepel, Y., Collangelo, M., Collins, S., Collamore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hegos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kanat, A., Karatas, A., Kelle, C., LaRocque, K., Lamazares, R., Landers, T., Leoczky, J., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Miho, T., Miengo, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schuback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Straus, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Triglio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission

Submitted (25-APR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

REFERENCE

AUTHORS

3 (bases 1 to 171914)
Birken, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavskiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y.,

Collamore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hegos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kanat, A., Karatas, A., Kelle, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Miho, T., Miengo, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schuback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Submitted (17-MAR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

On Mar 17, 2003 this sequence version replaced gi:25956367.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Web site: http://www-seq.wi.mit.edu

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L25499

Center clone name: 321 G 8

----- Summary Statistics

Sequencing vector: Plasmid; n/a; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 169262 bases at least Q40

Consensus quality: 170279 bases at least Q30

Consensus quality: 170654 bases at least Q20

Insert size: 176000; agarose-gel

Insert size: 170914; sum-of-contigs

Quality coverage: 10.1 in Q20 bases; agarose-gel

Quality coverage: 10.4 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently

* consists of 11 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.

* 1 13872: contig of 13872 bp in length

* 13873 13972: gap of 100 bp

* 13973 14646: contig of 674 bp in length

* 14647 14746: gap of 100 bp

* 14747 16119: contig of 1373 bp in length

* 16120 16219: gap of 100 bp

* 16220 17367: contig of 1148 bp in length

* 17368 17467: gap of 100 bp

* 17468 19014: contig of 1547 bp in length

* 19015 19114: gap of 100 bp

* 19115 31449: contig of 12335 bp in length

* 31450 31549: gap of 100 bp

* 31550 52958: contig of 21409 bp in length

* 52959 53058: gap of 100 bp

* 53059 70073: contig of 17015 bp in length

* 70074 70173: gap of 100 bp

* 70174 97112: contig of 26939 bp in length

* 97113 97212: gap of 100 bp

* 97213 132535: contig of 35323 bp in length

* 132536 132636: gap of 100 bp

* 132636 171914: contig of 39279 bp in length.

TITLE
JOURNAL

COMMENT

TITLE		TITLE	
JOURNAL		JOURNAL	
REFERENCE		COMMENT	
AUTHORS			

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* 26142 29590: contig of 3449 bp in length
* 29591 29690: gap of 100 bp
* 31311 31311: contig of 1621 bp in length
* 31312 31411: gap of 100 bp
* 31412 41665: contig of 10254 bp in length
* 41666 41765: gap of 100 bp
* 41766 54699: contig of 12934 bp in length
* 54700 54799: gap of 100 bp
* 54800 84383: contig of 29584 bp in length
* 84384 84483: gap of 100 bp
* 84484 112216: contig of 27733 bp in length
* 112217 112316: gap of 100 bp
* 112317 140050: contig of 27734 bp in length
* 140051 140150: gap of 100 bp
* 140151 175535: contig of 35385 bp in length
* 175536 175635: gap of 100 bp
* 175636 184032: contig of 8397 bp in length.
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FEATURES

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clone end:SP6
vector_side:left"
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misc_feature

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ORIGIN

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Query Match      52.3%; Score 29.8; DB 2; Length 184032;
Best Local Similarity 45.3%; Pred. No. 6.3e+02;
Matches 24; Conservative 15; Mismatches 14; Indels 0; Gaps 0;
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QY      2  GGUCCACUCCUGCGGUNNDNUGGCAUGCGGCUUGCGCAUGGCUAAGGGA 54
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      149817  GGTGACGCTCTTGAGGTGGGGGCTGGGGGGGGGTTCCTCTGGGTAGGGA 149869
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Search completed: May 19, 2004, 03:57:14
Job time : 3052 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 19, 2004, 02:59:41 ; Search time 390 Seconds
(without alignments)
663.253 Million cell updates/sec

Title: RIBOZYMEIA

Perfect score: 57

Sequence: 1 ggguccaccuccgcggun.....uucgcauggcuaggagccc 57

Scoring table: IDENTITY NUCDX

Gapop 10.0 , Gapext 1.0

Searched: 2947324 seqs, 2269024515 residues

Total number of hits satisfying chosen parameters: 5894648

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
- 16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
- 17: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
- 19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	29.6	51.9	52	13	US-10-150-407-40
2	29.6	51.9	52	13	US-10-150-407-80
3	29.6	51.9	52	16	US-10-346-880-40
4	29.6	51.9	52	16	US-10-346-880-80
5	29.6	51.9	90	9	US-09-733-042-12
6	29.6	51.9	90	9	US-09-733-042-13
7	29.6	51.9	90	10	US-09-190-246-2
8	29.6	51.9	91	15	US-10-237-302-7
9	29.6	51.9	99	15	US-10-237-302-8
10	29.6	51.9	8100	10	US-09-190-246-4
11	29.6	51.9	15538	10	US-09-190-246-1
12	29.2	51.2	466	10	US-09-918-595-2716
13	29.2	51.2	487	10	US-09-918-995-10300
14	29.2	51.2	601	14	US-10-109-860-6

c 15	29.2	51.2	1415	13	US-10-342-887-515	Sequence 515, Appl
c 16	29.2	51.2	1415	13	US-10-172-118-515	Sequence 515, Appl
c 17	29.2	51.2	1445	14	US-10-109-860-1	Sequence 1, Appli
c 18	29.2	51.2	9704	14	US-10-109-860-3	Sequence 3, Appli
c 19	29	50.9	564	15	US-10-029-386-4237	Sequence 4237, Ap
c 20	28.8	50.5	2730	15	US-10-156-761-178	Sequence 178, App
c 21	28.8	50.5	3300	16	US-10-260-238-1175	Sequence 1175, Ap
c 22	28.8	50.5	9025608	15	US-10-156-761-1	Sequence 1, Appli
c 23	28.4	49.8	3386	15	US-10-101-150-156	Sequence 156, App
c 24	28.4	49.8	3386	16	US-10-116-275-209	Sequence 209, App
c 25	28.4	49.8	3386	17	US-10-651-836-7	Sequence 7, Appli
c 26	28.2	49.5	56	10	US-09-507-362-39	Sequence 39, Appl
c 27	28.2	49.5	56	16	US-10-391-441-39	Sequence 39, Appl
c 28	28.2	49.5	1170	13	US-10-047-825-32	Sequence 32, Appl
c 29	28	49.1	372	13	US-10-085-783A-55374	Sequence 55374, A
c 30	28	49.1	372	16	US-10-242-535A-55374	Sequence 55374, A
c 31	28	49.1	1691139	15	US-10-067-514-1	Sequence 1, Appli
c 32	28	49.1	1691139	16	US-10-419-723-1	Sequence 1, Appli
c 33	27.8	48.8	842	15	US-10-252-157-493	Sequence 493, App
c 34	27.8	48.8	4711	15	US-10-084-817-183	Sequence 183, App
c 35	27.8	48.8	4732	15	US-10-433-013-17	Sequence 17, Appl
c 36	27.8	48.8	11009	9	US-09-845-583-1	Sequence 1, Appli
c 37	27.8	48.8	11009	15	US-10-037-182-3	Sequence 3, Appli
c 38	27.4	48.1	1519	13	US-10-047-825-7	Sequence 7, Appli
c 39	27.4	48.1	24081	15	US-10-132-134-13	Sequence 13, Appl
c 40	27.4	48.1	52101	15	US-10-132-134-1	Sequence 1, Appli
c 41	27.2	47.7	897	9	US-09-771-161A-26	Sequence 26, Appl
c 42	27.2	47.7	1200	16	US-10-369-493-24358	Sequence 24358, A
c 43	27.2	47.7	1218	13	US-10-282-122A-30258	Sequence 30258, A
c 44	27.2	47.7	1679	9	US-09-771-161A-25	Sequence 25, Appl
c 45	27.2	47.7	1956	17	US-10-416-314-101	Sequence 101, App

ALIGNMENTS

RESULT 1
US-10-150-407-40
; Sequence 40, Application US/10150407
; Publication No. US20040029278A1
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; Polo, John M.
; Jolly, Douglas J.
; Driver, David A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/150,407
; FILING DATE: 17-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/350,522
; FILING DATE: 08-Jul-1999
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423D1 / 1146.010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031

; INFORMATION FOR SEQ ID NO: 40:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 52 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 40:
 US-10-150-407-40

Query Match 51.9%; Score 29.6; DB 13; Length 52;
 Best Local Similarity 59.4%; Pred. No. 21;
 Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACUCCGCGGNNNNNUGGCGAUGC 35
 DB 1 TCCACCTCTCGGTCGACCTGGGCATCCG 32

RESULT 2

US-10-150-407-80
 ; Sequence 80, Application US/10150407
 ; Publication No. US20040029278A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dubensky Jr., Thomas W
 ; Polo, John M.
 ; Jolly, Douglas J.
 ; Driver, David A.
 ; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
 ; NUMBER OF SEQUENCES: 128
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SEED AND BERRY LLP
 ; STREET: 6300 Columbia Center, 701 Fifth Avenue
 ; CITY: Seattle
 ; STATE: Washington
 ; COUNTRY: US
 ; ZIP: 98104-7092
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/150,407
 ; FILING DATE: 17-May-2002
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/350,522
 ; FILING DATE: 08-Jul-1999
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: McMaisters, David D.
 ; REGISTRATION NUMBER: 33,963
 ; REFERENCE/DOCKET NUMBER: 930049.423D1 / 1146.010
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206) 622-4900
 ; TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 80:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 52 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 80:
 US-10-150-407-80

Query Match 51.9%; Score 29.6; DB 13; Length 52;
 Best Local Similarity 59.4%; Pred. No. 21;
 Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACUCCGCGGNNNNNUGGCGAUGC 35
 DB 1 TCCACCTCTCGGTCGACCTGGGCATCCG 32

RESULT 3
 US-10-346-880-40
 ; Sequence 40, Application US/10346880
 ; Publication No. US20030232035A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dubensky Jr., Thomas W
 ; APPLICANT: Polo, John M
 ; APPLICANT: Ibanez, Carlos E
 ; APPLICANT: Chang, Stephen M.W.
 ; APPLICANT: Jolly, Douglas J.
 ; APPLICANT: Driver, David A
 ; APPLICANT: Belli, Barbara A
 ; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
 ; FILE REFERENCE: PP01146.213 (CHIR-1146/11US)
 ; CURRENT APPLICATION NUMBER: US/10/346,880
 ; CURRENT FILING DATE: 2003-01-16
 ; PRIOR APPLICATION NUMBER: 09/503,138
 ; PRIOR FILING DATE: 2000-02-11
 ; PRIOR APPLICATION NUMBER: 09/191,747
 ; PRIOR FILING DATE: 1998-11-12
 ; PRIOR APPLICATION NUMBER: 08/739,199
 ; PRIOR FILING DATE: 1996-10-30
 ; PRIOR APPLICATION NUMBER: 08/404,796
 ; PRIOR FILING DATE: 1995-03-15
 ; PRIOR APPLICATION NUMBER: 08/376,184
 ; PRIOR FILING DATE: 1995-01-18
 ; PRIOR APPLICATION NUMBER: 08/348,472
 ; PRIOR FILING DATE: 1994-11-30
 ; PRIOR APPLICATION NUMBER: 08/198,450
 ; PRIOR FILING DATE: 1994-02-18
 ; PRIOR APPLICATION NUMBER: 08/122,791
 ; PRIOR FILING DATE: 1993-09-15
 ; NUMBER OF SEQ ID NOS: 128
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 40
 ; LENGTH: 52
 ; TYPE: DNA
 ; ORGANISM: Unknown
 ; FEATURE:
 ; OTHER INFORMATION: Artificial sequence: nested primer HDV17-68
 US-10-346-880-40

Query Match 51.9%; Score 29.6; DB 16; Length 52;
 Best Local Similarity 59.4%; Pred. No. 21;
 Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACUCCGCGGNNNNNUGGCGAUGC 35
 DB 1 TCCACCTCTCGGTCGACCTGGGCATCCG 32

RESULT 4

US-10-346-880-80
 ; Sequence 80, Application US/10346880
 ; Publication No. US20030232035A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dubensky Jr., Thomas W
 ; APPLICANT: Polo, John M
 ; APPLICANT: Ibanez, Carlos E
 ; APPLICANT: Chang, Stephen M.W.
 ; APPLICANT: Jolly, Douglas J.
 ; APPLICANT: Driver, David A
 ; APPLICANT: Belli, Barbara A
 ; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
 ; FILE REFERENCE: PP01146.213 (CHIR-1146/11US)
 ; CURRENT APPLICATION NUMBER: US/10/346,880
 ; CURRENT FILING DATE: 2003-01-16
 ; PRIOR APPLICATION NUMBER: 09/503,138
 ; PRIOR FILING DATE: 2000-02-11
 ; PRIOR APPLICATION NUMBER: 09/191,747
 ; PRIOR FILING DATE: 1998-11-12
 ; PRIOR APPLICATION NUMBER: 08/739,199
 ; PRIOR FILING DATE: 1996-10-30

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; PRIOR APPLICATION NUMBER: 08/404,796
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: 08/376,184
; PRIOR FILING DATE: 1995-01-18
; PRIOR APPLICATION NUMBER: 08/348,472
; PRIOR FILING DATE: 1994-11-30
; PRIOR APPLICATION NUMBER: 08/198,450
; PRIOR FILING DATE: 1994-02-18
; PRIOR APPLICATION NUMBER: 08/122,791
; PRIOR FILING DATE: 1993-09-15
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 80
; LENGTH: 52
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Artificial sequence: reverse primer HKV17-68
US-10-346-880-80

Query Match          51.9%; Score 29.6; DB 16; Length 52;
Best Local Similarity 59.4%; Pred. No. 21;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

Qy 4 UCCACCUCCGCGGUNNNNNUGGCGAUGCG 35
Db 1 TCCACCTCTCGCGTCCGACCTGGGCATCCG 32

RESULT 5
US-09-733-042-12
; Sequence 12, Application US/09733042
; Patent No. US20020168709A1
; GENERAL INFORMATION:
; APPLICANT: Hennecke, Frank
; TITLE OF INVENTION: Replicon Based Activation of Endogenous Genes
; FILE REFERENCE: 1700.0100001
; CURRENT APPLICATION NUMBER: US/09/733,042
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 60/169,988
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 90
; TYPE: DNA
; ORGANISM: HDV-FOR
US-09-733-042-12

Query Match          51.9%; Score 29.6; DB 9; Length 90;
Best Local Similarity 59.4%; Pred. No. 23;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

Qy 4 UCCACCUCCGCGGUNNNNNUGGCGAUGCG 35
Db 22 TCCACCTCTCGCGTCCGACCTGGGCATCCG 53

RESULT 6
US-09-733-042-13/c
; Sequence 13, Application US/09733042
; Patent No. US20020168709A1
; GENERAL INFORMATION:
; APPLICANT: Hennecke, Frank
; TITLE OF INVENTION: Replicon Based Activation of Endogenous Genes
; FILE REFERENCE: 1700.0100001
; CURRENT APPLICATION NUMBER: US/09/733,042
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 60/169,988
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 49
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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 90
; TYPE: DNA
; ORGANISM: HDV-REV
US-09-733-042-13

Query Match          51.9%; Score 29.6; DB 9; Length 90;
Best Local Similarity 59.4%; Pred. No. 23;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

Qy 4 UCCACCUCCGCGGUNNNNNUGGCGAUGCG 35
Db 73 TCCACCTCTCGCGTCCGACCTGGGCATCCG 42

RESULT 7
US-09-190-246-2
; Sequence 2, Application US/09190246
; Publication No. US20030180257A1
; GENERAL INFORMATION:
; APPLICANT: Parrington, Mark
; APPLICANT: Li, Xiaomao
; APPLICANT: Klein, Michel
; TITLE OF INVENTION: ALPHAVIRUS VECTORS FOR PARAMYXOVIRUS VACCINES
; FILE REFERENCE: Parrington et al.
; CURRENT APPLICATION NUMBER: US/09/190,246
; CURRENT FILING DATE: 1998-11-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 90
; TYPE: DNA
; ORGANISM: Semliki Forest virus
US-09-190-246-2

Query Match          51.9%; Score 29.6; DB 10; Length 90;
Best Local Similarity 59.4%; Pred. No. 23;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

Qy 4 UCCACCUCCGCGGUNNNNNUGGCGAUGCG 35
Db 22 TCCACCTCTCGCGTCCGACCTGGGCATCCG 53

RESULT 8
US-10-237-302-7
; Sequence 7, Application US/10237302
; Publication No. US20030119182A1
; GENERAL INFORMATION:
; APPLICANT: Alphavax, Inc.
; APPLICANT: Jonathan F. Smith
; APPLICANT: Kurt I. Kamrud
; APPLICANT: Jonathan O. Rayner
; APPLICANT: Sergey A. Dryga
; APPLICANT: Ian J. Calley
; TITLE OF INVENTION: ALPHAVIRUS REPLICON VECTOR SYSTEMS
; FILE REFERENCE: 01113.0002U2
; CURRENT APPLICATION NUMBER: US/10/237,302
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: 60/317,722
; PRIOR FILING DATE: 2001-09-06
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 91
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence; NOTE =
; OTHER INFORMATION: Synthetic Construct
US-10-237-302-7
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Query Match 51.9%; Score 29.6; DB 15; Length 91;
Best Local Similarity 59.4%; Pred. No. 23;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCCGCGGNNNNNUGGCGAUGC 35
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Db 18 TCCACCTCTCGCGTCCGACCTGGGCATCCG 49

RESULT 9

US-10-237-302-8/c
; Sequence 8, Application US/10237302
; Publication No. US20030119182A1
; GENERAL INFORMATION:
; APPLICANT: Alphavax, Inc.
; APPLICANT: Jonathan F. Smith
; APPLICANT: Kurt I. Kamrud
; APPLICANT: Jonathan O. Rayner
; APPLICANT: Sergey A. Dryga
; APPLICANT: Ian J. Caley
; TITLE OF INVENTION: ALPHAVIRUS REPLICON VECTOR SYSTEMS
; FILE REFERENCE: 01113.0002U2
; CURRENT APPLICATION NUMBER: US/10/237,302
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: 60/317,722
; PRIOR FILING DATE: 2001-09-06
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 99
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence; NOTE =
; OTHER INFORMATION: Synthetic Construct
US-10-237-302-8

Query Match 51.9%; Score 29.6; DB 15; Length 99;
Best Local Similarity 59.4%; Pred. No. 23;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCCGCGGNNNNNUGGCGAUGC 35
:||||:||||:||||:||||:||||:||||:||||:
Db 78 TCCACCTCTCGCGTCCGACCTGGGCATCCG 47

RESULT 10

US-09-190-246-4
; Sequence 4, Application US/09190246
; Publication No. US20030180257A1
; GENERAL INFORMATION:
; APPLICANT: Parrington, Mark
; APPLICANT: Li, Xiaomao
; APPLICANT: Klein, Michel
; TITLE OF INVENTION: ALPHAVIRUS VECTORS FOR PARAMYXOVIRUS VACCINES
; FILE REFERENCE: Parrington et al.
; CURRENT APPLICATION NUMBER: US/09/190,246
; CURRENT FILING DATE: 1998-11-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 8100
; TYPE: DNA
; ORGANISM: Semliki Forest virus
US-09-190-246-4

Query Match 51.9%; Score 29.6; DB 10; Length 8100;
Best Local Similarity 59.4%; Pred. No. 37;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCCGCGGNNNNNUGGCGAUGC 35
:||||:||||:||||:||||:||||:||||:||||:
Db 8032 TCCACCTCTCGCGTCCGACCTGGGCATCCG 8063

RESULT 11

US-09-190-246-1
; Sequence 1, Application US/09190246
; Publication No. US20030180257A1
; GENERAL INFORMATION:
; APPLICANT: Parrington, Mark
; APPLICANT: Li, Xiaomao
; APPLICANT: Klein, Michel
; TITLE OF INVENTION: ALPHAVIRUS VECTORS FOR PARAMYXOVIRUS VACCINES
; FILE REFERENCE: Parrington et al.
; CURRENT APPLICATION NUMBER: US/09/190,246
; CURRENT FILING DATE: 1998-11-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 15538
; TYPE: DNA
; ORGANISM: Semliki Forest virus
US-09-190-246-1

Query Match 51.9%; Score 29.6; DB 10; Length 15538;
Best Local Similarity 59.4%; Pred. No. 40;
Matches 19; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 4 UCCACCUCCGCGGNNNNNUGGCGAUGC 35
:||||:||||:||||:||||:||||:||||:||||:
Db 12479 TCCACCTCTCGCGTCCGACCTGGGCATCCG 12510

RESULT 12

US-09-918-995-2716/c
; Sequence 2716, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2716
; LENGTH: 466
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(466)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-2716

Query Match 51.2%; Score 29.2; DB 10; Length 466;
Best Local Similarity 50.0%; Pred. No. 37;
Matches 23; Conservative 13; Mismatches 10; Indels 0; Gaps 0;

QY 1 GGUCCACCUCCGCGGNNNNNUGGCGAUGC 46
:||||:||||:||||:||||:||||:||||:||||:
Db 99 GGGTGCTCTCTCGGACCTTGCTGTGTCATGGCGCTGCGGTGG 54

RESULT 13

US-09-918-995-10300/c
; Sequence 10300, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: Parrington et al.
; CURRENT APPLICATION NUMBER: US/09/190,246
; CURRENT FILING DATE: 1998-11-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 8100
; TYPE: DNA
; ORGANISM: Semliki Forest virus
US-09-190-246-4

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